Microsatellite DNA Analysis and Run Timing of Chinook Salmon in the White River (Puyallup River Basin)

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All genetic data for this study were collected and statistically analyzed by September 2000; as was information on historical patterns of Buckley trap arrivals and of historical tribal in-river fisheries. All of the above results were incorporated in an initial draft report that was circulated for review at that time. J. B. Shaklee presented an overview of the study results to the South Sound Spring Chinook Technical Committee at its November 1, 2000 meeting.

Review (both internal WDFW and external) and revisions of the draft report occurred thereafter until this final report was completed in October 2003.

Table of Contents

1

List Of Tables

List Of Figures

List Of Appendix Tables and Figures

Summary

We used data from 14 microsatellite DNA loci in five recent collections of chinook salmon in the Puyallup River system to characterize White River spring-run chinook salmon. Patterns of allele frequency variation and direct tests of population differentiation revealed that the two hatchery populations of White River chinook (at the White River Hatchery and at the Hupp Springs Hatchery) were genetically similar to each other but were very different from the Voights Creek Hatchery fall-run stock. In contrast, a collection of unmarked and untagged adults sampled at the Buckley trap on the White River in 1998 and a collection of naturally produced smolts collected in the lower White River in 2000 were each somewhat intermediate in their genetic characteristics (allelic composition and allele frequencies) to the spring-run and fall-run hatchery populations. Assignment of individual adults and of individual outmigrating smolts to their most unlikely stock-of-origin using the microsatellite DNA data indicated that both groups consisted of mixtures of fish of spring-run and fall-run origin (and/or contained fish of inter-stock hybrid origin). Estimates for each group were approximately 65-70% spring-run ancestry (and 30-35% fall-run ancestry).

We reviewed the historical patterns of arrival-timing exhibited by chinook in the White River using data from Buckley trap interception records from 1949 through 2000. This process revealed that the predominant pattern of chinook arrivals at the Buckley Diversion Dam (@ RM 24.3) from 1949 through 1970 was that of a spring-timed chinook run (majority of arrivals prior to July 1st) with a small percentage of fall-timed individuals (arrivals after September 30th). In contrast, substantial runs of later-timed chinook (average of 88% of the run arrived at Buckley after the second week in August) dominated the arrivals in the nine years from 1987 through 1995. Because the Buckley trap arrival patterns from 1971 through 1986 were much more variable and the run sizes from 1977 through 1986 were much smaller due to the intensive recovery program operations in these years, it was difficult to generalize about the nature of the chinook runs during this time period. Recent arrival patterns (1996 to present) showed a slightly increasing percentage of spring-timed fish and a concomitantly decreasing proportion of fall-timed fish at the Buckley trap. The increased numbers (and proportion) of spring-timed chinook and decreased proportion of summer/fall-timed chinook seen in the upper White River in the past five years may be attributable to successful spring-run chinook production by the multi-agency, hatchery-based White River Spring Chinook Recovery Program.

We also examined the patterns of estimated historical gillnet fishery harvests in the lower White and Puyallup Rivers in five selected years for information regarding patterns of run-timing. The temporal patterns of estimated catches in the years examined suggested that both spring-timed and fall-timed chinook runs were present in the lower White and/or Puyallup Rivers in 1954, 1955, 1957, 1966, and 1977. The timing of Buckley trap arrivals and the temporal patterns of these estimated fishery harvests suggested to us that the fall-timed chinook were confined to the lower White River (below the Buckley trap) from 1954 through 1977 (except in 1973). Whether or not a native fall-timed chinook run occurred in the upper White River prior to 1954 is unclear, but Buckley trap counts for 1949 - 1953 suggest this possibility.

Although the basis for the appearance of the fall-timed run in the years since 1977 is unknown, increased minimum in-stream flows since 1987 and/or changes in hatchery operations may well have contributed to this change.

Given that there is little evidence that the fall-timed chinook run observed in the upper White River in the last 20 or so years is native to this system, we are concerned about the potential for interbreeding and/or competition between the presumed native White River spring-run stock and these fall-timed fish.

Introduction

White River Basin and the History of Chinook in the White River

The White River originates in the glaciers of Mt. Rainier and flows 68 miles before its confluence with the Puyallup River near the city of Sumner, Washington (Appendix Fig. 1). A number of natural and anthropogenic events have affected the White River and its indigenous fish species (Appendix Table 1). Among the most important events has been the construction of two dams, the Buckley Diversion Dam and the Mud Mountain Dam. The Buckley Diversion Dam was built on the White River at river mile (RM) 24.3 in 1911. Diversion of water from an approximately 20-mile stretch of the river and the altered stream flows in the lower river that resulted from the Dam's construction and operation are believed to have been significant impediments to passage and rearing of chinook salmon (WDFW et al., 1996). Soon after the dam was completed, a fish ladder was built to allow upstream adult migration (Bob Barnes, Puget Sound Energy, personal communication, Oct. 31, 2000). This ladder remained in operation until at least 1941. Construction of the Mud Mountain Dam at RM 29.6 (1940-1948) completely blocked upstream fish passage. Because of this, the U.S. Army Corps of Engineers (USACE) replaced the fish ladder on the Buckley Diversion Dam with a fish trap and commenced trap and haul operations in 1940 to pass adult salmonids from the Buckley trap to the upper White River above Mud Mountain Dam (to a site at approximately RM 33.6). It is the trap and haul operations at the Buckley diversion dam that have provided the counts of arriving chinook that we have analyzed to document both historical abundance and run-timing of White River chinook.

Key events affecting the characteristics of the White River watershed and the chinook stocks occurring in it are summarized in Appendix Table 1.

The 1992 Salmon and Steelhead Stock Inventory (SASSI) (Washington Department of Fisheries et al., 1993) recognized both spring and summer/fall chinook stocks native to the White River. Past accounts have reported a population of fall-timed chinook spawning in the lower White River, between RM 3.5 and 24.3 (Williams et al., 1975). Neither the overview by Williams et al., nor the 1993 SASSI document, provide any count data affirming the presence or abundance of this putative stock although both sources describe its migration and spawn timing, and the locations of fall-timed stock spawning in the upper river are mapped in the SASSI document. The Williams et al. report does not, however, mention any spawning of fall-timed chinook in the upper White River. Thus, whether or not a distinct summer/fall stock ever existed in the upper White River (above the location of the Buckley trap) and, if so, whether or not it still exists are matters of some uncertainty.

There have been a number of documented plants of fall-run chinook hatchery stocks in many locations in the Puyallup River basin. Large numbers of Soos Creek (formerly Green River) Hatchery fall chinook were planted into the Puyallup River and its tributaries until the late 1980s (Washington Department of Fisheries et al., 1993). Although direct transfers of out-of-basin chinook have been discontinued, the fall-run stock propagated at Voights Creek Hatchery, which is the source of more recent plants, is itself predominantly of Soos Creek origin. Hatchery

origin, fall-run chinook have also been introduced into the White River on several occasions. There were a series of Washington Department of Fish and Wildlife (WDFW) releases of fall-run chinook from both the Soos Creek and Voights Creek Hatcheries into the White River between 1952 and 1957 and three releases by the Puyallup Tribe from the Puyallup Tribal Hatchery in 1982 (Appendix Table 2). Whether or not any of these releases between 1952 and 1982 produced significant numbers of returns in subsequent years is unknown. We did not find documentation of any other releases of fall-run chinook into the White River in more recent years in WDFW planting record databases or in the Pacific States Marine Fisheries Commission (PSMFC) Regional Mark Information System.

Another potential source of non-native fish is chinook immigration or "straying." Because many hatchery stocks (including Voights Creek fall-run) were untagged or tagged at very low rates historically, there are few data that directly address straying levels into the upper White River. In 1998, no out-of-basin coded wire tagged fish were observed at the Buckley trap. In 1999 (the first year that Voights Creek Hatchery fall chinook were tagged), a total of only 13 strays were detected (Appendix Table 3).

The White River spring-run chinook stock had declined from an average annual escapement of just over 2,950 (1942-1950 average) to less than 500 fish by the late 1950s, presumably largely because of juvenile and adult passage problems and habitat degradation (Salo and Jagielo, 1983 and WDFW et al., 1996). The pattern of this decline is shown graphically in Figure 1. The counts of chinook at the Buckley trap and the numbers of fish harvested in the lower Puyallup and White river fisheries are documented in Appendix Table 4. This pronounced decline in abundance was the impetus for initiating recovery efforts for the White River spring chinook stock.

Overview of Hatchery Propagation and the White River Spring Chinook Recovery Program

White River spring-run chinook were utilized in at least three different programs involving artificial propagation (reviewed by Appleby and Keown, 1995). The first of these programs was part of the Washington Department of Fisheries "Thirteen Point Plan" for restoring the South Puget Sound sport fishery. This effort took place in 1971 and 1972 and involved the hybridization of White River male chinook with female Green River, Issaquah Creek, and Hood Canal fall chinook and with Cowlitz River spring chinook. The resulting inter-stock hybrid progeny were released in several Puget Sound locations (not including the White River) and in Hood Canal. Small numbers of female White River chinook were inadvertently included among the males taken from the White River in both years and these were spawned with White River males. The pure stock progeny resulting from these crosses in 1971 were apparently released from the Voights Creek Hatchery, judging by an otherwise unexpected return of spring-timed chinook to this hatchery in 1975. The pure stock progeny resulting from these crosses in 1972 were released at the Minter Creek and Voights Creek Hatcheries. This program almost certainly had no direct positive effects on the White River spring-run chinook stock because the progeny of the majority of fish removed from the White River (males) were released in other watersheds to enhance the sport fishery, not returned to the White River.

The second project was directed at restoring the White River spring-run chinook stock and took place from 1974 to 1976. It involved artificial spawning of White River male and female chinook and the eventual planting of the resulting yearling smolts back into the White River. We believe that this project also probably had little or no positive effect on the status of the White River spring-run chinook stock because: a) there were relatively high pre-spawning mortalities and/or fry losses in the hatchery; and b) because the progeny of the largest brood (1976) had bacterial kidney disease (BKD) and likely had low survival rates (internal WDF memo from C. Baranski to B. Gerke, August 2, 1978). A third reason to expect little positive effect from these years is the very low observed tag recovery rate. There was only a single terminal-area tag recovery (at the Voights Creek Hatchery) from the total of 48,865 progeny (100% coded wire tagged) that were planted from the Recovery Program in 1974 and 1975 (data from PSMFC Regional Mark Information System). The 1976 brood progeny were not tagged (because of BKD) so we have no comparable return numbers for this brood.

As a result of the continuing decline in the numbers of White River spring-run chinook and concern that extinction of the stock was imminent, fish were captured at the Buckley trap in 1977 and transported to the Minter Creek Hatchery for artificial spawning and rearing. Progeny from these fish were used in two recovery programs cooperatively undertaken by the National Marine Fisheries Service (NMFS), the Puyallup Tribe, the Muckleshoot Tribe, and WDFW (reviewed by Appleby and Keown, 1975; WDFW et al., 1996). One program, conducted at the WDFW Minter Creek Hatchery (and a satellite facility, Hupp Springs Hatchery) reared the progeny to fingerling or yearling size before release to complete the anadromous component of their life cycle. Adults returning 3-5 years later were spawned with additional fish captured at the Buckley trap and the cycle repeated. The second program, conducted at the Manchester facility of the NMFS, reared the fish in saltwater net pens until maturation. The combined efforts of these programs resulted in a substantial increase in the number of returning adults, and in 1997, spawning of adults at the Manchester facility was terminated. The numbers of fish used in each program are shown in Appendix Figures 1 and 2 and Appendix Table 4.

Releases of spring chinook into the White River were initiated as the number of returning adults increased, and with the completion of the White River Hatchery in 1989. The White River Hatchery has played a major role in the recovery program by producing and releasing pre-smolts both directly from the hatchery and from acclimation ponds in the upper White River. Fish from these releases are expected to return as adults to the Buckley trap or the White River Hatchery trap on the White River. In early years, the hatchery-produced pre-smolts released into the upper White River were untagged and/or unmarked. These untagged and unmarked fish (especially those from the acclimation ponds) are expected to be more or less indistinguishable from naturally produced chinook in the basin (and some of them may have been included in either the sample of adults from the Buckley trap in 1998 or the sample of outmigrant smolts in 2000 that were analyzed in this study).

Genetics

Genetic data can be used to characterize populations, investigate population divergence and interrelationships, and estimate the stock composition of mixed samples. For the past 20 years, the electrophoretic analysis of allozyme variation has been used to characterize salmon

populations (for example, see Gharrett et al., 1994) and to provide estimates of stock contributions in salmon mixed-stock fishery applications (see, for example: Pella and Milner, 1987; Shaklee et al., 1999).

Allozyme analyses have been conducted over the past 10+ years on a number of Washington chinook salmon collections, both for the populations making up the White River Spring Chinook Recovery Program and for many other Puget Sound stocks, and the results of many of these studies in relation to the White River Recovery Program have been previously summarized (WDFW et al., 1996). These studies have addressed such issues as the distinctiveness of the "spring-run" populations propagated in the hatchery/captive broodstock operations of the recovery program (vs. fall-run stocks) and the stock origin(s) and relationships of both unmarked adults arriving at the Buckley trap in the White River and of naturally produced smolts outmigrating from the White River. However, the levels of variation typically observed for allozyme markers have been insufficient to allow stock-specific estimates of mixture proportions or individual stock-of-origin assignments.

The analysis of DNA variation, particularly for markers such as microsatellites that typically exhibit high numbers of alleles and high heterozygosities, may provide increased power to characterize stocks, estimate interrelationships among populations, and analyze mixtures. Microsatellite DNA loci are tandemly repeated arrays of short (commonly di-, tri-, and tetra-nucleotide) sequences occurring commonly in eukaryotic organisms (Wright and Bentzen, 1994). Microsatellites generally consist of arrays less than 300 base pairs in size, and allelic variation is commonly due to variation in the number of times the basic repeating unit occurs (thus, microsatellite alleles are typically distinguished and named according to their size). Microsatellites are considered to be non-coding in that they do not encode RNA or proteins. Because microsatellites are non-coding, allelic variation at microsatellite DNA loci is assumed to be selectively neutral. Microsatellite DNA variation typically exhibits biparental, Mendelian inheritance (e.g., Ardren et al., 1999) and alleles are co-dominantly expressed allowing an organism's genotype to be unambiguously inferred from its DNA phenotype. However, some microsatellite loci have so-called null alleles that do not yield a detectable product. Microsatellite loci with null alleles are, therefore, more difficult to use because an individual's genotype cannot be unambiguously inferred from its microsatellite phenotype.

A growing number of studies have used variation at microsatellite DNA loci to investigate stock structure (Small et al., 1998; Beacham et al., 1999; Beacham and Wood, 1999; Shaklee et al., 1999). Microsatellite variation has also been shown to provide a basis for assigning unknown individuals to their population-of-origin based on the individual's multilocus genotype and differences in allele frequency distributions among the possible source populations (Paetkau et al., 1995; Rannala and Mountain, 1997; Shriver et al., 1997; Smouse and Chevillon, 1998; Cornuet et al., 1999; Olsen et al., 2000).

Because these DNA markers offer the potential of higher resolution analyses, we initiated a study of microsatellite DNA variation in White River chinook to characterize five groups of fish relevant to the recovery program: 1) the White River spring-run population at the White River Hatchery; 2) the White River spring-run population at the Hupp Springs Hatchery; 3) the fall-run stock at the Voights Creek Hatchery; 4) unmarked adults arriving at the Buckley trap on the

White River; and 5) naturally produced smolts emigrating from the White River. We also used the microsatellite DNA data to attempt to assign individual Buckley trap adults and outmigrating smolts to their most likely stock-of-origin. We attempted the latter application to investigate whether or not it would be possible to use these markers to provide improved monitoring and evaluation capabilities with which to assess past, current, and future chinook stock restoration activities in the basin.

Microsatellite DNA loci are valuable genetic markers not only because of their high levels of genetic variability but also because they (like other DNA markers) can be analyzed using fin clip and other non-lethal biopsy samples. Non-lethal methods may prove to be essential for this application because of the critically low abundance of the White River spring-run chinook stock and the fact that Puget Sound chinook salmon have been listed for protection under the Endangered Species Act by the National Marine Fisheries Service.

Objectives of the Present Study

This study was undertaken to determine the genetic interrelationships among different groups of White River chinook. Specifically, we wanted to determine whether or not the unmarked, untagged adult chinook arriving at the upper White River watershed and the naturally produced smolts emigrating from the White River were "pure" spring-run chinook or were a mixture of spring-run and summer/fall-run stocks. Additionally, we wanted to use the genetic data, together with information on adult arrival timing at the Buckley trap, to gain insights regarding the historic and current run-timing and stock identity of chinook in the White River and of the genetic effects of the White River Spring Chinook Recovery Program.

Materials and Methods

Collections Analyzed

We analyzed the following samples:

Collection (life history stage & collection year)	Collection Location	Sample Code	Number of Fish
WDFW Hupp Springs Hatchery (adults; 1998)	Hatchery	98CP	99
White River Tribal Fish Hatchery (adults; 1998)	Hatchery	98CO	100
WDFW Voights Creek Hatchery (adults; 1998)	Hatchery	98CQ	98
White River unmarked (adults; 1998)	RM 24.3[a]	98CB	105
White River natural (smolts; 2000)	RM 5.9[b]	00BE	101

[a] = U.S. Army Corps of Engineers adult trap on the White River near Buckley (RM 24.3)
[b] = WDFW outmigrant smolt trap on the lower White River at approximately RM 5.8 - 6.0

In general, fish at the hatcheries were sampled on multiple days throughout the spawning period as they were used for spawning. At Hupp Springs Hatchery, approximately equal numbers of males and females were sampled as follows – 9/15/98: n=20; 9/22/98: n=28; 9/29/98: n=34; 10/6/98: n=15; and 10/12/98: n=2. At White River Hatchery, approximately equal numbers of males and females were sampled as follows – 9/10/98: n=20; 9/17/98: n=50; 9/24/98: n=20; 10/1/98: n=20; 10/8/98: n=10. At Voights Creek Hatchery, fish were sampled as follows – 9/22/98: n=18; 9/24/98: n=18; 9/29/98: n=14; 10/1/98: n=14; 10/6/98: n=18; 10/8/98: n=6 (sexes of fish sampled were not recorded).

The general intent for the sampling of unmarked adults at the Buckley trap was to subsample representatively throughout the run. However, although the first chinook arrived at the trap on May 25th, DNA sampling didn't begin until July 8th, after approximately one-fifth of the run had passed the trap. Comparison of the pattern of adult arrivals with the subsample that was taken for DNA analysis revealed that the sample used for DNA analysis had no representation in the first four weeks of the run and that it under-represented the fifth, sixth, and sixteenth and seventeenth weeks. Despite these shortcomings, we concluded that the sample used for DNA analysis covered most of the arrival timing and could be considered to provide a reasonable representation of the adult run in 1998. No age or sex data are available for any of the fish in this sample (but the dates that individual samples were collected are shown in Table 5). The general intent for the sampling of naturally produced smolts was to sample smolts proportionately once per week throughout the period of outmigration. Because there were both hatchery-origin and naturally-produced chinook smolts in the White River, we attempted to exclude all of the hatchery-origin smolts from our sample. This was done by excluding marked/tagged smolts. All fish produced at, and released from, the White River Hatchery were coded-wire tagged (CWT). Therefore, we tested each smolt with a portable CWT detector and excluded any fish that caused a positive reading on the detector from our sample. Approximately 98.5% of the 380,900 hatchery-origin smolts released from the two acclimation ponds in the upper White River (released on June 9, 2000) had their left pelvic fin removed as a visual mark (unpublished data

from Blake Smith, Puyallup Tribe). All smolts at the trap were visually examined for this fin mark and marked individuals were excluded from our sample. Given these marks and the sampling procedures that were used, we believe that our sample of "naturally"-produced smolts likely contained at most one or two hatchery-origin fish. The actual smolt samples were obtained opportunistically on five different days from May 10th through June 20th, as fish were available. Based on the sizes of the smolts in the DNA sample, they were all presumed to be zero-age (although a small percentage of larger, presumed yearling smolts were trapped during the season).

DNA Methods

Genomic DNA was extracted by digesting a small piece of fin tissue in a 5% chelex (BioRad Chelex 100 resin) solution containing proteinase K (Sigma). Following extraction at 65EC for 30-180 min, the samples were heated for five minutes at 95EC to denature proteins. A small portion of each resulting DNA extract was diluted as needed to enable polymerase chain reaction (PCR) amplification of the microsatellite loci. The dilutions were stored at 5EC until all analyses had been completed.

We amplified the microsatellite DNA loci of interest via the polymerase chain reaction (PCR; see Saiki et al., 1988) using fluorescently labeled primers (obtained from Applied Biosystems or Integrated DNA Technologies). Our protocols for PCR amplification were modified from those of Jeff Olsen, Alaska Dept. of Fish and Game, Anchorage, AK and Terry Beacham, Department of Fisheries and Oceans, Nanaimo, B.C. Canada) or other published protocols. Wherever feasible, we multiplexed loci together at the PCR step and/or on gels (Olsen et al., 1996) to increase efficiency and decrease costs. Details regarding the primers and protocols we used for PCR amplification are summarized in Appendix Table 5.

We used data for all loci screened in our analyses; except *Ots-102*, which is known to exhibit significant heterozygote deficiencies in many populations (Young and Shaklee, 2000a & b); presumably due to the presence of one or more null alleles. Data were collected using an ABI-377 semi-automated sequencer.   Applied Biosystems software (ABI-Collection, GeneScan v.3.0, and Genotyper v.2.0) were used to collect and analyze the raw data to determine genotypes at each locus (based on estimated size in base pairs). The output tables from Genotyper were imported into MS Excel where allele calling was accomplished using size bins defined based on the repeat motif of each microsatellite and the observed distributions of raw Genotyper size calls for each locus.

Statistical Methods

We used the program GENEPOP v.3.2a (see Raymond and Rousset, 1995a) to: a) calculate descriptive statistics such as allele frequencies and genotypic proportions; b) test Hardy-Weinberg equilibrium expectations; and c) test for population differentiation (Raymond and Rousset, 1995b) among the collections. We used the program WHICHRUN (v. 4.0 beta) (Banks and Eichert, 2000) to assign individual smolts to their most likely stock-of-origin and then adjusted these assignments using a maximum likelihood procedure developed by S.F. Young (as described in Young and Shaklee, 2000a).

Analysis of Arrival Timing

We consulted two types of data to assess the temporal patterns of historical chinook spawning migrations into the White River. We hoped the patterns in the data would resolve the uncertainty about whether in the past the White River was a spawning area for two stocks of chinook salmon, a spring-run stock and a fall-run stock, or only a single, spring-run stock. The first type of data, trap and haul records from the Buckley Diversion Dam, provided an informative view of the timing of fish that made it into the upper drainage. However, that picture by itself was incomplete because fish produced in the basin were exposed to multiple anthropogenic and natural factors, including river flows too low to allow adult upstream migration and fishery harvests in saltwater and in the lower river. One or more of those factors could result in few fish returning to the Buckley trap. The second type of data, catch estimates from in-river fisheries, were particularly useful because they could be used to infer the timing of spawning migrations. Those catch estimates represented only an unknown proportion of total fishery harvest and therefore did not enable us to estimate relative impacts of those fisheries on the populations; however, they allowed us to examine the temporal patterns of chinook spawning migrations passing through those fisheries, and provided information that helped to resolve the uncertainty about whether only a single spring-timed stock or both a spring-timed stock and a fall-timed stock historically spawned in the basin.

Analysis of Trap and Haul Records

We used U.S. Army Corps of Engineers (USACE) Buckley Diversion Dam trap and haul records as the source of information regarding the numbers and arrival times of chinook at the trap. Because the diversion dam consists of panels designed to collapse during high flows, it may not be an absolute barrier to upstream adult migration at these times. However, despite collapsed panels during high flow events, the high water velocities at such times, together with the geometry of the dam and associated downstream apron and approach, may actually prevent passage. Whether this dam represents an absolute barrier to upstream passage or is somewhat less effective, we believe that fish counts at the dam provide a reliable and informative data set that can be used to document the magnitudes and temporal patterns of adult chinook return to that point in the White River.

Because we could find no official records for the earliest years of trap operations (1949-1973) at WDFW and the Corps of Engineers staff we contacted (Larry Crain and Jeff Dillon) had no knowledge of the existence of such records, we relied on the hand-written, weekly summary Buckley trap information (originally obtained from USACE) that is maintained by the WDFW Habitat Program for the years 1954-1973. Count data for the years 1949-1953 are from the annual summary numbers of the USACE. We used official copies of USACE weekly reports for our analysis of these counts for the more recent years (1974-2000). Although the recent USACE weekly reports itemize counts on a daily basis, the earlier years' data summaries only reported weekly counts. Therefore, we only used weekly counts to allow consistent analyses across all years. Because the week ending dates used in the USACE records didn't correspond to the same Julian dates from year to year, there was minor year-to-year variation in the reporting periods. Additionally, our summaries of run timing based on periods such as "before week ending including July1" and "after week ending including Sept. 30" often included or excluded several

days counts because the cutoff date we used did not occur at the beginning or end of a USACE weekly reporting period.

We combined the counts for "jacks" (2-year old males) with those for adults for three reasons. First, there were no counts of jacks in the USACE records prior to 1976, and it was unclear to us whether this lack of counts resulted from their true absence in these years or because the USACE made no attempt to distinguish them in those years. Second, because jacks are likely to make reproductive contributions to the next generation they are truly a part of the population. Third, because the distinction between jacks and adults can be somewhat arbitrary and might not have been applied consistently from year to year we did not view this distinction as reliable in this data set. We included all chinook data from the USACE records in the time period of interest in our analysis (which were done after entering the counts into MS-Excel spreadsheets). We looked over the records carefully and attempted to correct apparent errors when the counts were internally inconsistent or when there was other information that indicated to us that a tabulated USACE count was in error. We have noted the cases where we concluded that the USACE count was erroneous in footnotes to Appendix Table 4.

We looked for major changes in arrival timing for all years from 1949 through 2000 by categorizing the percentage of the total arrivals for the year that occurred in each of three time periods: 1) prior to July 1 or prior to the week ending that included July 1st; 2) after the 2nd week in August; and 3) after September 30 or after the week ending that included September 30. We considered the earliest of these periods to be an indication of spring-timed chinook, the latest to be an indication of fall-timed chinook, and the middle to be an ambiguous or potentially mixed period. For a number of arbitrarily selected years, we also plotted the weekly counts and subjectively interpreted the resulting patterns to draw inferences and make conclusions about the patterns of arrival timing within and among years.

Analysis of Historical Terminal-Area Fisheries Catch Estimates

We used the WDFW salmon fishery catch statistics for our analysis of historical net fisheries in the White and Puyallup Rivers. Records of catch for both the lower White River fishery conducted by the Muckleshoot Tribe and the lower Puyallup River fishery conducted by the Puyallup Tribe were reviewed. These records were assembled by WDFW from information provided to the Department by the tribes and/or information collected by WDFW staff as part of the agency's attempts to document fishery harvests throughout Washington.

Most of this historical information is only available in bound, printed volumes (i.e., they are not presently computerized). These volumes can be accessed at the WDFW headquarters in Olympia, WA.

When we first accessed and used this historical catch information, we believed that it represented actual numbers of fish caught. However, at least one reviewer of an earlier draft of this report expressed doubts about the accuracy of these numbers. We, therefore, contacted Mr. Dale Ward (an employee of the Washington Department of Fisheries from 1956 until 1989 who collected much of this information and supervised the agency's catch recording process for many years) for information about these records. He informed us that, despite their appearance in the records,

the numbers recorded as numbers of fish harvested in the lower Puyallup and White Rivers were not actual counts, but were indexes. According to Mr. Ward, these were derived from information gathered during infrequent visits (often only once or twice per month) by WDFW staff to these rivers to interview selected tribal fishers on the White River and a single fish buyer on the Puyallup River. The information gathered during these visits was then extrapolated to generate **indexes** of daily harvests that were tabulated as official catch records. While this new perspective regarding these catch records suggested to us that the records couldn't be used quantitatively, we believed that the indexes were, nevertheless, useful and informative in helping to discern historical patterns of run-timing of chinook returning to the White River and we used them in this manner. We believe, however, that the accuracy of these harvest indexes is uncertain and that caution must be used when interpreting them.

We had access to lower White River tribal fishery harvest indexes for the years 1943 to 2000, and lower Puyallup River tribal harvest indexes from 1954 to 2000. However, we only had annual harvest indexes for the lower White River tribal fishery for 1943 - 1949. Furthermore, we only analyzed the temporal patterns of harvest indexes for a subset of the years for which daily catch indexes were available. Specifically, we analyzed harvest indexes for most of the same years that we had plotted weekly Buckley trap arrival data for (see above) so that we could use the fishery harvest indexes to help us understand the Buckley trap arrival data better.

Results

Characteristics of the Hatchery Spring-Run vs. Fall-Run Populations

The 14 loci used in the analyses had moderate to high levels of variation (number of alleles per locus ranged from 7 for *Ots-1** to 29 for *Ssa-197**). While most alleles were observed in all five collections, allele frequencies were noticeably different among stocks at most loci (Table 1). Inspection of the allele frequency distributions revealed differences of 0.1 or more between the Voights Creek Hatchery fall-run stock and one or both of the hatchery spring-run populations (White River Hatchery and Hupp Springs Hatchery) for selected alleles at several loci (*One-8*170* and **182*; *Ots-3*90* and **92*; *Ots-1*188* and **192*; *Ots-108*172*; *Ots-107*179,* and **239*; *Ogo-2*224*; *Ots-101*192* and **216*; *Ocl-1*162* and **174*; *Ots-2*71, *81,* and **105*; *Ogo-4*137* and **161*; *Str-73*127*; *Ots-104*212*; *Ssa-197*208* and **236*) as shown in Table 1 and Figure 2.

Characteristics of Adults at the Buckley Trap and of Outmigrating Smolts

Allele frequencies in the collection of unmarked adults sampled at the Buckley trap and/or the collection of outmigrating naturally produced smolts were approximately intermediate between the frequencies in the fall-run hatchery stock and those in the spring-run hatchery populations for many of the alleles that showed the largest frequency differences between the spring-run and the fall-run populations (e.g., *One-8*170*; *Ots-1*188* and **192*; *Ots-2*81* and **105*; *Ogo-4*137* and **161*; *Ots-101*192* and **216*; *Ocl-1*174;* cf Table 1 and Figure 2). These intermediate frequencies in the arriving adults and in the outmigrating naturally produced smolts suggest that both of these groups of fish may be mixtures of spring-run and fall-run fish and/or may contain substantial numbers of fish of mixed spring x fall ancestry (= inter-stock "hybrids").

The presence or absence of rare alleles in population samples can sometimes provide insight into population interrelationships. However, the reliability of such inferences is directly related to sample sizes because sampling error for detecting very rare alleles becomes large in small samples. Nevertheless, an examination of the allele frequency data shows several interesting trends in the presence/absence of rare alleles in the five collections analyzed in this study.

There were several rare alleles in the unmarked adults arriving at the Buckley trap and/or in the outmigrating naturally produced smolts that were seen in the Voights Creek Hatchery fall-run stock but were not observed in either of the spring-run hatchery populations (White River Hatchery and Hupp Springs Hatchery) – *One-8*156*; *Ots-3*78, *98,* and **100*; *Ots-108*144* and **168*; *Ots-2*73* and **99*; *Ogo-4*147* and **157*; *Str-73*155*; *Ots-107*267* and **303*; *Ots-101*152, *176,* and **244*; *Ocl-1*166*; *Ots-104*276, *280,* and **288*; *Ssa-197*172, *220,* and **256* (Table 1). Collectively, these data suggest that there are fall-run origin chinook arriving at the Buckley trap and/or spawning in the White River watershed.

Although rare, several (11) alleles were seen in the unmarked adults arriving at the Buckley trap that were not observed in either of the spring-run hatchery populations (White River Hatchery

and Hupp Springs Hatchery) or in the Voights Creek Hatchery fall-run stock – *Ots-3*84*; *Ots-108 *164*, *Ots-2*65*; *Str-73*159*; *Ots-107*275*; *Ots-101*252* and **272*; *Ocl-1*154*; *Ots-104*200* and **296*; *Ssa-197*164*. Similarly, several (13) rare alleles were observed in the White River naturally produced outmigrant smolts but not in the fall-run or spring-run hatchery populations (*One-8*166*; *Ots-3*84* and **88*; *Ots-1*198*; *Ots-2*63*; and **109*; *Str-60*136*; *Ogo-4*131* and **135*; *Str-73*159*; *Ots-107*291*; *Ots-101*252*; *Ssa-197*112*). However, two of the rare alleles (*Ogo-4*131* and *Ssa-197*112*) in the smolt collection were found in the homozygous state in the same smolt. Based on its genotype at these loci, and the lack of amplification at three additional loci, this smolt was determined to be a coho and omitted from subsequent analyses. Another smolt exhibited a total of four alleles not seen in any of the four adult collections, but all of these alleles were present in the heterozygous state. Because the second allele at each of these four loci was observed in most or all of the other collections, and often at relatively high frequencies, it seems likely that this smolt was a chinook. Whether or not one or both of its parents were "strays" from an out-of-basin stock is unknown.

It is difficult to know how much attention to pay to the occurrence and distribution of rare alleles because their presence or absence may simply be reflective of the low probability of encountering them in relatively small sample sizes. Alternatively, the presence of rare alleles not observed in any of the baseline populations might be due either to straying of fish from out-of-basin stocks into the upper White River or to year-class variability in allele content in the spring-run and/or fall-run populations. While it seems unlikely to us (given the relatively high level of interest in, and study of, White River chinook over the past 25+ years), it is also true that the possible existence of an additional, undocumented native chinook stock in the upper watershed could account for these rare alleles.

Ten loci exhibited frequency differences of 0.08 or greater between the two hatchery spring-run populations (White River Hatchery and Hupp Springs Hatchery) for certain alleles – *One-8*170*; *Ots-3*96*; *Ots-2*71*; *Ots-107*179*; *Ots-101*224*; *Ots-104*212*; *Ogo-2*238*; *Str-60*140*; *Ogo-4*141*; *and Str-73*139* – suggesting that even these two populations may have diverged significantly from each other (see below).

Tests of Hardy Weinberg Equilibrium & Genetic Differentiation

Tests of Hardy-Weinberg equilibrium expectations at the 14 loci screened in the three hatchery populations and in the White River outmigrant smolt collection (Table 2) yielded non-significant deviations in all but 3 of 56 tests (after adjustment of the " -level for multiple testing in each collection; " = 0.05/14 = 0.0036). We interpret the general agreement with Hardy-Weinberg equilibrium expectations at these loci in the four collections as an indication that the observed data fit the model of simple Mendelian inheritance with co-dominant expression of alleles used to interpret observed microsatellite DNA phenotypes in this study. Furthermore, we interpret the general lack of deviations from Hardy-Weinberg genotypic proportions as an indication that each of the four samples of fish in these collections could represent a randomly interbreeding parental population.

In contrast, the collection of unmarked adults arriving at the Buckley trap in 1998 had two loci (*Ots-107** and *Str-60**) that were significantly out of Hardy-Weinberg equilibrium and two

additional loci (*Ssa-197** and *Ogo-4**) that were nearly significantly out of Hardy-Weinberg equilibrium (unadjusted p values of 0.0078 and 0.0039, respectively). In all four cases, the deviations were due to deficiencies of heterozygotes. We believe that these results are an indication that adult chinook from at least two different stocks (presumed spring-run and fall-run) arrived at the White River in 1998 (see discussion below).

We tested for significant genetic differences among the collections by using the approach of Raymond and Rousset (1995b). The results of a test of genic differentiation among all Pairwise combinations of the five collections are summarized in Table 3. Because a total of 10 Pairwise tests were done, we tested the significance of the results by using an " < 0.05 level (adjusted for multiple tests; " = 0.01/10 = 0.005). When this was done, nine of the 10 Pairwise comparisons of populations (using 14 loci) yielded significant outcomes. The comparison between the two hatchery spring-run populations yielded a P value of 0.011, which was not statistically significant after the adjustment for multiple tests.

Because of concerns that the observed deviations from Hardy Weinberg equilibrium expectation noted above might bias some of the tests of genic differentiation (which assume Hardy Weinberg equilibrium), we also conducted several pair-wise tests of genotypic differentiation. The results of these tests are shown in Table 4. A test of the White River Hatchery spring-run population vs. the Hupp Springs Hatchery spring-run population yielded a statistically significant outcome over all loci (P = 0.0177) even though none of the 14 loci yielded a significant difference (adjusted " - level = 0.05/14 loci = 0.0036). Taken together, these test outcomes are somewhat ambiguous and we believe that the tests should be repeated with samples from other years before reliable conclusions can be drawn about the relationship of these two hatchery spring-run populations. In contrast, comparisons between the collection of unmarked adults arriving at the Buckley trap and: 1) the White River Hatchery spring-run population; 2) the Hupp Springs Hatchery spring-run population; 3) the Voights Creek Hatchery fall-run stock; or 4) the White River naturally produced smolts, all had P values over all 14 loci of less than 0.001. Statistically significant differentiation was noted between both the Hupp Springs Hatchery and the White River spring-run populations and the Voights Creek Hatchery fall-run stock (with an overall P value of 0.0000 and significant differences at 13 of the 14 loci in each case). The comparisons between either the unmarked adults that arrived at the Buckley trap or the outmigrant smolts and all three hatchery populations indicated significant differences as well. Finally, the comparison between the unmarked Buckley trap adult collection and the White River naturally produced smolt collection yielded a significant overall test result (unadjusted P = 0.0003), even though none of the 14 individual loci showed a significant difference between these two collections.

Assignment of Naturally Produced Smolts to Their Stock-of-Origin

Because the tests of genetic differentiation revealed substantial differences among populations, we used the program WHICHRUN (which assigns unknowns to their most likely stock-of-origin based on multilocus genotype probabilities) to investigate the genetic affinities of the unmarked adults that arrived at the Buckley trap on the White River in 1998 and of the naturally produced smolts (Year-2000 outmigrants) with regard to spring-run vs. fall-run genetic ancestry. We used a baseline where the White River Hatchery spring-run population, and the Hupp Springs Hatchery spring-run population represented spring-run ancestry, and fall-run ancestry was

represented by the Voights Creek Hatchery fall-run stock. This analysis assigned 34 smolts to the White River Hatchery spring-run population, 31 smolts to the Hupp Springs Hatchery spring-run population, and 35 smolts to the Voights Creek Hatchery fall stock. These numbers remained unchanged when the maximum likelihood adjustment developed by SFY was applied. Thus, before and after adjustment, 65 of the naturally produced smolts were assigned spring-run origin and 35 were assigned fall-run origin. We plotted log-likelihood ratios (LLR) of multilocus genotype frequencies (likelihood of spring-origin divided by likelihood of fall-origin according to Shriver et al., 1997) against collection date to provide a graphical depiction of the results (Figure 3). In this plot, the LLRs of fish assigned fall-origin were multiplied by -1 to clarify the graphical representation. The results reveal little evidence of a pronounced difference in outmigration timing between smolts classified as spring-run and those classified as fall-run, except that the latter group is somewhat under represented in the latest sample (Figure 3).

It is important to note that artificially reared smolts were released from the White River Hatchery between May 25th and June 7th and some of these were collected at the smolt trap. All smolts produced at this hatchery had been coded-wire tagged before release, and all smolts in the sample were run through a tag detector so that all individuals carrying a coded wire tag (CWT) could be identified and removed from the genetic sample. Nevertheless, it is possible that a few smolts could have lost their tags (CWT loss rates for chinook tagged as zero-age pre-smolts are typically less than 5%; Gary Schurman, WDFW personal communication 16 April, 2001). Therefore, an attempt was made to identify any hatchery-origin smolts by visual examination of body shape; and a small number of presumed hatchery-origin smolts were removed from the genetic sample using this process. Hatchery-produced smolts emigrating from the acclimation pond could also have been sampled at the smolt trap but, because these were 100% marked with a ventral fin clip in 2000, we don't believe that any of these were included in the sample for DNA analysis. We are confident that the resulting sample of smolts that was analyzed contained very few, if any, hatchery-origin fish.

Only two of the eight chinook smolts having alleles not observed in any of the three baseline populations were classified as spring-run; the other six were classified as fall-run. Although these proportions are roughly the inverse of what would be expected if these smolts were a random subsample of all smolts analyzed, the significance of this observation is unclear.

Assignment of Unmarked Adults at the Buckley Trap to Their Stock-of-Origin

We also conducted a similar analysis of the collection of unmarked adults that arrived at the Buckley trap in 1998. The WHICHRUN analysis of this collection assigned 38 adults to the White River Hatchery spring-run population, 36 adults to the Hupp Springs Hatchery spring-run population, and 31 adults to the Voights Creek Hatchery fall-run stock. When the adjustment developed by SFY was applied to these original assignments from WHICHRUN, final assignments of: 43 adults to the White River Hatchery spring-run population, 31 adults to the Hupp Springs Hatchery spring-run population, and 31 adults to the Voights Creek Hatchery fall stock were obtained. Thus, for the adults arriving at the Buckley trap in 1998, both unadjusted and adjusted values were 74 spring-run origin and 31 fall-run origin. These results are summarized in some detail in Table 5, which also shows the stock assignment, date of capture,

and the number of loci successfully scored for each fish. Nine of these unmarked adults carried one or more alleles not observed in any of the three baseline populations. Five of these were classified as spring-run and four were classified as fall-run. These proportions are close to the proportions observed in the total adult sample.

While the reliability of stock-of-origin assignment undoubtedly declines as the number of loci scored in an individual diminishes, this does not seem to have resulted in a systematic bias in our results given that, of the fish with fewer than nine loci successfully scored, nine individuals were classified as spring-run (64%) and five were classified as fall-run (36%). An interesting, but not unexpected, pattern in the data is that the majority of the individuals classified as spring-run were relatively early arrivals to the trap whereas the majority of those classified as fall-run were relatively late arrivals (Figure 4; LLRs calculated and plotted as described above for the plot of stock-of-origin assignment for the smolt sample).

Evaluation of Stock-of-Origin Assignments

We tested our stock-of-origin assignments in two ways. First, we treated the sample from one of the two hatchery spring-run populations as unknowns and assigned them to their presumed stock-of-origin using WHICHRUN with a baseline that consisted of only the Voights Creek Hatchery fall-run stock and the other spring-run hatchery population. The results of this analysis when the fish from the White River Hatchery spring run population were treated as unknowns were: 83 fish assigned by WHICHRUN to the Hupp Springs Hatchery spring-run population and 7 fish assigned to the Voights Creek Hatchery fall-run stock (10 fish lacked genetic data). After the WHICHRUN assignments were adjusted using the method of SFY, the assignments were 90 to the Hupp Springs Hatchery spring-run population and zero fish assigned to the Voights Creek Hatchery fall-run stock. The reciprocal test with the fish from the Hupp Springs Hatchery spring-run population treated as unknowns yielded: 96 fish assigned by WHICHRUN to the White River Hatchery spring-run population and 3 fish assigned to the Voights Creek Hatchery fall-run stock (1 fish lacked genetic data). After these WHICHRUN assignments were adjusted using the method of SFY, the assignments were 97 to the White River Hatchery spring-run population and 2 fish assigned to the Voights Creek Hatchery fall-run stock. Clearly this analysis suggests that the assignment methodology (especially after adjustment) is robust given the present data set.

We also conducted simulations to investigate the performance of the assignment analysis using 'fish' (artificially created multilocus genotypes) of known stock origin as unknowns. All simulations were done using two simplifying assumptions: 1) genotypes at all loci were in Hardy Weinberg equilibrium proportions; and 2) all simulated 'fish' had complete multilocus genotypes (i.e., no missing data). In the actual data sets, we know that genotypes were not in Hardy Weinberg equilibrium in all cases (c.f. Table 2) and that there were individuals missing data for one or more loci (in fact, in some collections there were many individuals that were missing data at a few loci; e.g., see Table 5).

We simulated three mixture scenarios, performing 100 iterations per scenario and simulating 100 fish per iteration. The three scenarios were of "mixtures" simulated as: 1) 100 White River Hatchery spring chinook; 2) 100 Hupp Springs Hatchery spring chinook; and 3) 100 Voights

Creek Hatchery fall chinook. Each iteration involved two resamplings (with replacement) of each of the potential source population baseline genotype data sets. The first resampling provided an estimate of allele frequencies that we used in conjunction with a random number generator to simulate an "unknown mixture" of fish. The second resampling provided an independent estimate of baseline population allele frequencies. We used those baseline population frequencies to generate an expected frequency for each genotype observed in the mixture in each of the potential source populations. Simulation results are summarized in Table 6.

Under all three scenarios the average unadjusted WHICHRUN assignments erred by less than 2% when spring-run vs. fall-run was the criterion, while the average adjusted assignments erred by no more than 0.3%. Average mis-assignment rates between the two spring-run hatchery populations were considerably higher for both unadjusted (14.8 - 25.8%) and adjusted assignments (1.4 - 8.4%), especially when the source of the simulated "unknown mixture fish" was the Hupp Springs Hatchery population. The reason for the observed asymmetry in stock-of-origin assignments between these two spring-run hatchery populations is unknown at present. We believe the assignment accuracy that we achieved in these simulations supports our use of the maximum likelihood stock of origin assignment method in this study.

Historical Patterns of Arrival Timing of Chinook at the Buckley Trap

The demonstration that approximately 30% of the unmarked and untagged adults arriving at the Buckley trap on the White River in 1998 and roughly 35% of the naturally produced smolts emigrating from the lower White River in 2000 were of fall-run ancestry was initially quite a surprise to us given the intent and operation of the White River Spring Chinook Recovery Program. Indeed, the results of the DNA-based stock-of-origin assignments initially led us to suspect that the program had been recently compromised by the intrusion of one or more fall-run stocks. Therefore, we investigated this possibility by reviewing the historical patterns of arrival timing exhibited by chinook in the White River. Although arrival patterns at the Buckley trap could have been, and probably were to some extent, influenced by variable in-stream flows, we assumed that differences in arrival times of several weeks or more were likely to indicate real biological differences. The question being tested by the following analysis was whether or not there was clear evidence of both spring-timed and fall-timed chinook arrivals at the Buckley trap in past years; the null hypothesis being that chinook only arrived in significant numbers at the Buckley trap during the spring period (i.e., before July 1st).

Pattern of arrival in 1998

The first step in our review of these records was to investigate the pattern of arrival timing exhibited by the adults that arrived at the Buckley trap in 1998, the year that our sample of unmarked adults was taken, to see whether or not the sample of arriving adults obtained for DNA analysis was temporally representative of that run. As shown in Figure 5, adult chinook arrived at the Buckley trap beginning with the week ending May 30th and the run didn't stop until the week ending October 24th.

This plot provided a suggestion of three pulses of fish, one peaking in mid July, one peaking in mid August, and a third peaking at the end of September – beginning of October. About 11% of the 402 chinook seen at the Buckley trap in 1998 arrived before July 1st, about 51% after the second week in August, and only about 4% arrived after the weekending that included or directly followed September 30th. This pattern of arrival is not expected for a "typical" spring-run population because of the large proportion of late-arriving fish and because of its multi-peak profile. For example, NF Nooksack spring chinook exhibit a unimodal, early timed arrival pattern (Nooksack Spring Chinook Technical Group, 1987). Indeed, the strong, sharp peak of fish from late September through early October is much more typical of fall-timed chinook stocks (e.g., the bulk of the Voights Creek Hatchery fall-run chinook arrive at the hatchery rack after the first week of September; unpublished WDFW hatchery records).

Patterns of Arrival in Other Years

We then investigated the temporal pattern of adult arrivals at the Buckley trap in other years to see whether or not the run in 1998 was typical for chinook in the White River. First we investigated Buckley trap arrival timing in all years from1949 through 2000 by calculating the percentage of the year's run in three periods: period 1, arrival prior to July 1 (which we considered to represent typical spring-timed chinook); period 2, after the second week of August (a time when late-arriving spring-run and/or early arriving fall-run chinook might be expected); and period 3, after September 30 (which we considered to indicate fall-run chinook). The results of this analysis are shown in Table 7. We believe that these analyses reveal five different periods, each characterized by a different basic pattern of arrival timing (excluding the ten years during which the recovery program was actively removing early-timed chinook from the White River; 1977-1986): 1) prior to 1954; 2) 1954 to 1970; 3) 1971 through 1976; 4) 1987 through 1995; and 5) 1996 through 2000.

The first of these periods was prior to 1954 when from 5% to 22% of the chinook hauled from the Buckley trap into the upper watershed arrived at the Buckley trap after the end of September. Absolute abundances of fall-timed chinook in those years ranged from 37 to 151 individuals versus 270 to 940 spring-timed individuals.

In the second of these periods (1954 to 1970), the run consisted of an average of 60% arrivals before July 1, only about 6% after the second week in August, and less than 1% after September 30. We consider the run during this period to have exhibited a typical spring-timed arrival pattern.

The pattern of return in the third period (1971 through 1976) was characterized by an average of only 24% of the run before July 1, about 23% after the second week in August, and an average of 3% of the run after September 30. We believe that the decreased percentage of the run prior to July 1 and increased proportion after the second week of August are consistent with the presence of fall-timed chinook in the return.

We recognized two more phases after 1986. From 1987 through 1995, the run averaged less than 3% of arrivals prior to July1, just under 88% after the second week of August, and about 17%

after September 30. We see little evidence of a strong spring-timed run in these numbers and a clear indication of an abundance of late summer or fall-timed chinook.

The most recent phase consists of the 1996 through 2000 returns, during which an average of just over 6% of the chinook arrived prior to July 1, about 48% arrived after the second week of August, and just over 3% arrived after September 30. Thus, this last phase shows a decline in late-timed arrivals (after the second week of August) and a slightly increased spring-timed component.

We also plotted the pattern of weekly arrivals at the Buckley trap for many of the years from 1954 through 2000. The patterns for the most recent years (1996 - 2000) clearly revealed that chinook arrived at the Buckley trap in multiple pulses over a broad time period in each of these years (Figure 6). Indeed, the timing of the earliest peak of arrivals during this 5-year period was consistent with that typically exhibited by so-called spring-run chinook stocks in western Washington (e.g., April - July for Suiattle, upper Cascade, and Sol Duc stocks; WDFW et al., 1993). The timing of the latest peak of arrivals was similar to that typically shown by so-called fall-run chinook stocks. The patterns of arrival timing exhibited from 1996 to 2000 suggested that multiple stocks of chinook (with different run timings) were present in the White River throughout this period. However, on average for this 5-year period, less than 7% of the Buckley trap arrivals occurred before July 1st and over 3% occurred after September 30th.

The plots of weekly arrival timing in the years from 1978 to 1995 showed that chinook arrivals at the Buckley trap were dominated by a single, late-timed peak (early-September to mid-October) (Figure 7). Of the years during this time period that we plotted (1978, 1981, 1987, 1988, and 1990-1995), there were only two years when more than 10% of the total run arrived earlier than July 15th (15.7% in 1978 and 23.8% in 1981). In some of these years (1993, 1991, and 1987), less than 3% of the total run arrived prior to July 15th. It is worth noting that the removal of most of the spring-timed chinook arriving at the Buckley trap from 1977 to 1986 to implement the Recovery Program (Appendix Table 4) and the fact that the progeny produced in the Recovery Program were not returned to the White River until 1987 (Appleby and Keown, 1995) undoubtedly contributed to this pattern of late arrival (because these fish are not included in the Buckley trap counts because they were not hauled above the trap). On average for the 10 years that we plotted during this 18-year period, only 3% of the Buckley trap arrivals occurred before July 1st and over 19% occurred after September 30th.

The patterns of arrival timing for the White River chinook run in period 2 (1954-1970 and period 3 (1971-1976) were somewhat similar. In all years plotted (1954, 1957, 1965, 1966, 1975, 1976, and 1977), the peak week was no later than July 10th (Figure 8). During these seven years, over 65% of the total run had arrived by July 15th in all years except 1975 (when only 40% had arrived by this date). These patterns of arrival timing are more typical of that displayed for so-called spring-run chinook stocks in western Washington (see above). On average for these seven years during this 24-year period, 48% of the Buckley trap arrivals occurred before July 1st and less than 1% occurred after September 30th. Thus, based on the years between 1954 and 1977 that we graphed, there was little or no evidence of a substantial post-September 30th (fall-timed) peak. Indeed, we conclude that the White River chinook counted at the Buckley trap from 1954 through 1970 appeared to be predominantly or entirely a spring-timed run.

However, we conclude that the Buckley trap records provide convincing evidence of a fall-timed chinook run in the years from 1978 through 1995 and some evidence for it in the years from 1996 through 2000. Therefore, we reject the null hypothesis that only spring-timed chinook arrived in significant numbers at the Buckley trap during these two time periods.

Information from In-River Fishery Harvest Indexes of White River Chinook Runs

The varied patterns of arrival timing at the Buckley trap documented above were enigmatic because they suggested the possibility of profound changes in chinook migration timing and possibly in stock composition (e.g., the proportions of spring-run vs. fall-run stocks) in the upper White River over the past 45 years. Although chinook returns during this time were undoubtedly affected by habitat and environmental conditions (e.g., in-river flows) and by marine fisheries harvests, we could not find any data documenting these effects on White River chinook. Therefore, we examined the patterns of in-river fishery harvest indexes in selected years during this time period in an attempt to document and understand the temporal aspects of White River chinook spawning migrations better.

Two tribal fisheries were relevant to this analysis. One was a Puyallup tribal fishery in the lower Puyallup River, which occurred basically from Commencement Bay to the confluence of the White River with the Puyallup River (RM 10.4). The majority of effort in this fishery was concentrated from RM 5.7 to the mouth of the Puyallup River (B. Smith, Puyallup Tribe, personal communication on 3 November, 2000). Because this fishery occurred below the confluence with the White River, it could well have intercepted salmon destined for the White River (as well as Puyallup River fish). However, because of the likely mixed-stock nature of this fishery, its impact on White River salmon runs was difficult to estimate with confidence. The Muckleshoot Tribe conducted the second relevant fishery in the lower White River. This latter fishery presumably only intercepted salmon destined to spawn in the White River (because of its location) and, thus, its relationship to Buckley trap arrivals (and White River salmon runs) was presumably straightforward. For this reason, the analyses and descriptions below are focused more on the White River tribal fishery harvest indexes, although harvest indexes for the lower Puyallup River fishery are described as well. We did not analyze the fishery harvest indexes to conduct an explicit hypothesis test, rather, we analyzed them to see whether or not they were consistent with the Buckley trap counts and to see if we could gain additional insights regarding the magnitude and timing of historical White River chinook runs.

The catch indexes (in records at WDFW) for both of these fisheries often had no or very small numbers for August and/or early September. Whether or not there were catches during this time period could not be confidently determined but, if they did occur, our analyses would underestimate fishery effects during this time period. If they did not occur, fish destined for the upper White River would presumably have been accounted for by the Buckley trap arrival numbers during this period (with a lag period due to transit time), whereas fish destined to spawn in the lower White River (below the Buckley trap) would not show up in the Buckley trap counts. It is noteworthy, however, that in some years (e.g., 1957) at least one of these two fisheries had substantial catch indexes during the August - September time period.

The total annual Buckley trap arrival numbers are plotted with the annual commercial tribal harvest indexes of the White River fishery to allow estimation of the minimum run of chinook to the White River in Figure 9. The estimates of sport fishery harvests in the White River were not included in the estimates of minimum White River chinook run size because the punch card data upon which the sport catch estimates were based were very limited and incomplete (the maximum estimated sport catch was 33 chinook in 1990; see Appendix Table 4). It is clear from Figure 9 that the estimated tribal in-river fishery harvests in many years were relatively large compared to the total run. The actual numbers for both the Buckley trap arrivals and for the in-river fishery harvest indexes can be found in Appendix Table 4.

We also plotted the Buckley trap arrival counts together with tribal in-river fishery catch indexes for selected years to examine the effects of the fisheries on the pattern of arrival timing. The plot for Buckley trap arrival numbers (count = 633) and Muckleshoot White River tribal fishery catch indexes (estimated total N = 1,271) in 1954 indicates that there were substantial numbers of both spring-timed and fall-timed chinook in the White River (Figure 10A & B). Buckley trap counts showed that about 36% of the chinook arrived before July 1st and less than 4% arrived after September 30th while the White River tribal fishery indexes suggest that about 58% of the harvest occurred prior to July 1st and 39% occurred after September 30th. Taken together, these numbers suggest that both spring-timed and fall-timed chinook were present in the lower White River, but that only the spring-timed run entered the upper White River (based on the pattern of Buckley trap counts). Alternatively, if some of the spring-timed chinook held in the lower river until after September 30th they could have accounted for the late fishery catches rather than the presence and harvest of a fall-timed stock.

We also believe that the harvest indexes for the lower Puyallup River fishery conducted by the Puyallup Tribe in 1954 are of considerable relevance to understanding the White River chinook run (Figure 10C). This fishery apparently harvested a considerable proportion of spring-timed fish (over 18% before July 1st and 91% by July 16th). Given that there is no recognized spring-run chinook stock in the Puyallup River (WDFW et al., 1993), we believe that all of these fish were White River spring chinook. The stock origin(s) of the 7% fall-timed fish harvested in this fishery after August 14th is less clear, because the fish could have been of either White River or Puyallup River origin.

Similar analyses were conducted for the 1955, 1957, 1966, and 1977 chinook runs. In 1955, 202 chinook arrived at the Buckley trap before July1 while only 6 arrived after September 30th (see Figure 11). Approximately 27% and 38% spring-timed chinook were apparently harvested in the lower White River and lower Puyallup River tribal fisheries in 1955, and about 64% fall-timed chinook were estimated to have been harvested in October in the lower White River fishery. Thus, while both spring-timed and fall-timed chinook runs appeared to have been present in the lower White River in 1955, only the spring-timed run entered the upper river (as evidenced by the Buckley trap counts).

The numbers and patterns for chinook in 1957 are illustrated in Figure 12. The Buckley trap counts were dominated by spring-timed chinook in 1957, with about 78% of the fish arriving before July 1st and about 1% arriving after September 30th (Figure 12A). The estimated harvests in the White River fishery in this year suggest that about 12% of the fish were caught before July

1st (spring-timed) and that over 50% were caught after September 30th (fall-timed) (Figure 12B). There were no estimated catches of chinook prior to July 15th in the lower Puyallup River fishery in this year, but large numbers of chinook were apparently caught throughout August and September. The profiles shown in this figure again demonstrate that the chinook run to the White River was composed of two primary components; one spring-timed and the other fall-timed although only the spring-timed component appears in the Buckley trap counts.

Because there were no estimated chinook harvests in the lower Puyallup River tribal fishery in 1966, we have only examined Buckley trap arrival numbers (N = 639) and estimated Muckleshoot White River tribal fishery catches (N = 1,772) for this year (Figure 13). About 38% of the fish that arrived at the trap arrived before July 1st, about 58% arrived in July, and no fish arrived after September 30th. Over 42% of the estimated tribal harvest in the White River in 1966 occurred before July 1st and about 47% occurred after September 30th. If the estimated White River fishery catch is combined with the Buckley trap arrivals, it seems clear that the 1966 run was composed of both spring-run and fall-run stocks but that only the spring-timed run entered the upper White River (based on the Buckley trap counts).

The results of similar analyses for the 1977 run are shown in Figure 14. Although estimated total numbers of chinook were considerably reduced compared to those in previous years, the general patterns were similar to those described above for other years. While many of the fish that arrived at the Buckley trap in 1977 were taken to the recovery program, when these are combined with those actually passed above the trap, 58% of the chinook arrivals at the trap occurred prior to July 1st and none occurred after September 30th (Figure 14A). Very few chinook were estimated to have been harvested in the Muckleshoot lower White River fishery in 1977 (N = 23). All of those fish were caught after September 14th, and about 75% of these were caught after September 30th. Despite this small number, this estimated harvest suggests the presence of a fall-timed chinook run in the White River in this year (Figure 14B). All of the tribal harvests in the lower Puyallup River in 1977 consisted of fish caught after September 15th, a portion of which might have been destined for the White River (Figure 14C).

We believe that the results described above suggest that the chinook run to the White River consisted of both spring-timed and fall-timed fish in most years between 1954 and 1977 but that very few fall-timed fish entered the upper White River (only very small numbers arrived at the Buckley trap).

White River Hatchery Returns vs. Buckley Trap Counts in 1996 and 2000

We plotted the numbers of adults hauled above the Buckley trap and the numbers of White River Hatchery returning adults for 1996 and 2000 (Figure 15). These plots reveal several interesting features. In 1996, 412 fish returned to the White River Hatchery and 715 chinook arrived at the Buckley trap. Thus, the total chinook return to the upper White River was made up of 37% White River Hatchery fish and 63% Buckley trap fish. In 1996, only 5% of the total Buckley trap arrivals occurred before July 1st, whereas 9% of the total White River Hatchery return had arrived by this date.

In contrast, the 209 chinook that returned to the White River Hatchery in 2000 constituted only 12% of the total run to the upper White River (1,546 fish arrived at the Buckley trap). In 2000, less than 27% of the arrivals at the Buckley trap occurred by July 1st, whereas 39% of the White River Hatchery returns had arrived by this date. The tail ends of these runs were also different, with only 7% of the White River Hatchery return occurring after September 2nd but 31% of the Buckley trap arrivals coming after this date. We interpret these data as evidence that the adult chinook arriving at the Buckley trap in 1996 and 2000 showed a smaller percentage of early-timed fish and a significantly larger proportion of late-arriving fish than did the White River Hatchery spring-run stock returns in both years and, although the White River Hatchery population is considered a "pure spring-run stock", over 90% of the returns in 1996 and over 60% of the returns in 2000 occurred after July 1st. This contrasts with the general pattern observed prior to 1971.

Discussion

Comparison of Microsatellite DNA Results with Past Allozyme Results

Past allozyme-based genetic characterizations of collections taken in 1991, 1992, and 1993 from the Hupp Springs freshwater/anadromous hatchery component and the South Sound Net Pen saltwater captive broodstock component of the White River Spring Chinook Recovery Program led to four conclusions: 1) these populations were not statistically significantly different from each other in any of these three years; 2) statistically significant differences were observed between all pairs of annual collections when collections from the two sources in each year were pooled and the resulting aggregates were tested; 3) the various White River spring chinook collections were more similar to one another than any of them were to other Puget Sound chinook stocks despite these year-to-year differences, and, in fact; 4) White River spring chinook were significantly different from other Puget Sound spring-run and fall-run chinook stocks (A. Marshall internal WDFW memo of October 6, 1994 regarding White River [Puyallup] spring chinook genetic analysis; Marshall et al., 1995; WDFW et al., 1996 and A. Marshall, WDFW, personal communication).

The microsatellite DNA results from this study are consistent with the above conclusion that the two hatchery populations of White River spring-run chinook are much more similar to one another than either is to fall-run chinook (although we only compared the spring-run hatchery populations to the Voights Creek Hatchery fall-run stock). Because we have not included DNA data for any other Puget Sound chinook stocks in this analysis, we cannot say how the White River spring-run populations compare to other chinook stocks in the region.

The results of our DNA-based analyses of the Year-2000 smolt collection, however, contrast with the results of an allozyme analysis of 1995 outmigrating smolts (A. Marshall, WDFW, memo of April 10, 1996 to the South Sound Chinook Technical Committee regarding the 1995 White River juvenile chinook outmigrant sample). In her analysis of 39 allozyme loci in a sample of 88 smolts, Marshall reported finding "No significant differences ($p > 0.05$) in allele frequencies..." between the smolt sample and the sample from the captive brood program, although the smolt sample was significantly different from a sample of Puyallup Hatchery (= Voights Creek Hatchery) fall-run chinook. The DNA-based stock-of-origin assignment analysis of the sample of Year-2000 outmigrating smolts (Figure 3) shows that this sample was composed of both spring-run and fall-run origin fish and this result is consistent with the demonstration of significant differentiation (DNA markers) between the Year-2000 smolt sample and the spring-run hatchery populations (tables 3 and 4). Comparing these two different outcomes, it is tempting to conclude that there has been a major genetic change in the smolts produced in the White River between 1995 and 2000 (and, by inference, in the parental populations that produced them; primarily 1994 and 1999, respectively). There are, however, several other possible reasons for this observed difference.

The different outcomes from the allozyme testing of the 1995 smolt sample and the DNA testing of the Year-2000 smolt sample could have resulted from sampling fundamentally different smolt populations because the two smolt collections were made at different locations and different

times in the two years. The 1995 smolt sample was collected immediately downstream of the Dingle Basin fish collection facility (which is isolated from the White River by gradient) in the bypass reach below the Buckley Dam at approximately RM 21 between June 5th and June 28th. The Year-2000 smolt sample was collected in the by-pass reach of the lower White River at approximately RM 5.9 between May 10th and June 20th using a smolt trap. Thus, the Year-2000 sample could have included smolts produced by spawning in the lower White River below the Buckley Dam whereas the 1995 smolt sample could not have included any smolts produced in the lower river. Furthermore, sixty-nine of the 101 smolts in the Year-2000 sample were collected before May 26th whereas none of the smolts in 1995 were collected before June 5th. The differences between the allozyme and DNA results could also have been due to differences in the power of the two data sets and analyses, year-to-year differences in the genetic characteristics of the smolt populations sampled in the two different years (due to genetic drift and/or field sampling error), and/or a combination of these factors. Unfortunately, we cannot determine the relative roles played by these or other factors from existing information. However, allozyme analysis of the Year-2000 smolt sample is pending and may shed some light on this issue.

Implications of Observed Variation in Arrival Timing at the Buckley Trap

The graphical analysis of temporal patterns of adult arrival timing revealed substantial variability among years, with the pattern for any individual year falling into one of three basic patterns: spring-timed, fall-timed, or complex-multipeaked. We interpret these results as evidence of important changes in the chinook runs arriving at the Buckley trap over this approximately 45-year period. We believe that these data provide compelling evidence that the chinook arriving at the Buckley trap in the 1950s and 1960s basically consisted of a single, spring-timed run. By the 1970s, the pattern of arrival-timing at the Buckley trap had become more variable from year-to-year, with mid-summer and fall peaks occurring in some years, suggesting either the possible intrusion of non-native fish from one or more fall-run stocks into the upper White River, random variation in arrival timing within the depressed spring-run stock, or the reappearance of a fall-timed stock that had existed in the system prior to 1954.

Another possible explanation would be a relatively recent divergence from a single, unimodal run-timing to two components (spring-run and fall-run) induced by changes in the White River drainage in the past 100 years (see Quinn and Unwin, 1993; Quinn et al., 2000; Hendry et al., 2000). While we have no direct information bearing on this issue, we believe this alternative interpretation is unlikely based on the DNA characterizations of the smolts and of the returning adults at Buckley which have suggested that most of these fish have genotypes similar to those in the White River spring-run hatchery stock but approximately one-third have genotypes similar to those in the Voights Creek fall-run hatchery stock. Indeed, there is no *a priori* reason to expect that recent divergence in run timing would result in microsatellite DNA genotypes at many loci that are more like those of fall-run stocks such as the Voights Creek Hatchery stock than of the original White River spring-run stock.

The numbers of arriving adults in most years during the late 1970s and the1980s were so low that it is risky to draw any inferences regarding the pattern of arrival timing during this period.

Nevertheless, late-timed chinook dominated Buckley trap arrivals during the period from 1981 to 1995. In contrast, Buckley trap arrivals in the five most recent years exhibited a much more protracted time of arrival, with two or three peaks in each year. The earliest of these three peaks coincides rather closely with the time of Buckley trap arrival exhibited by White River chinook in the 1950s and 1960s (Figure 8) and the latest with the return timing of most fall-run stocks. It is tempting to speculate that the presence and increasing abundance of spring-timed adults at the Buckley trap in recent years is the consequence of the success of the White River Spring Chinook Recovery Program.

Inferences from Terminal-Area Fishery Harvest Indexes

The analysis of estimated timing and catch indexes of the two relevant in-river fisheries (in the lower Puyallup River and in the lower White River) clearly suggests that the run of chinook to the lower White River had both spring-timed and fall-timed components in the earliest years analyzed (1954, 1955, 1957, 1966, and 1977).

We caution, however, against inferring too much of an effect by these terminal-area fisheries on the timing or numbers of chinook observed at the Buckley trap in any given year. While we believe that these historical fishery harvest indexes provide useful insights regarding the timing and magnitude of lower White River chinook runs, other factors such as: a) habitat changes; b) low, modified, and/or fluctuating flow regimes; and c) marine fisheries undoubtedly had large (but undocumented) impacts. However, because many of the relevant data were either never collected, or have been lost through time, we will probably never have a full understanding of most of these other effects.

A recurring pattern seen in the five years of estimated fishery catch indexes and Buckley trap counts from 1954 to 1977 that we plotted (1954, 1955, 1957, 1966, and 1977) is that very few fall-timed chinook made it to the Buckley trap (and therefore into the upper White River) in any of these years. The patterns seen in these five years suggest that the terminal area fisheries in the lower Puyallup and White Rivers harvested the vast majority of the late-returning chinook in most years during this period and/or that the vast majority of late-run fish that escaped the fisheries did not ascend as far upstream as the Buckley trap, for whatever reason. If this general pattern persisted throughout the entire time period between 1954 and 1977, as is suggested by the data in Table 7, the source of the large numbers of fall-timed chinook observed in the upper White River after 1977 is unclear.

This raises the question of whether or not the current fall-run chinook population in the White River (defined by the microsatellite DNA results, not just by run-timing) is actually native to this river system or has become established relatively recently (perhaps via immigration from one or more nearby native populations or via straying from one or more hatchery populations). Alternatively, did conditions change in such a way that the very small numbers of fall-timed chinook seen at the Buckley trap in several years from 1954 to 1977 gave rise to the considerably larger fall-timed populations observed from 1978 to present? If the current fall-timed population arriving at the Buckley trap is native to the White River, whether or not it remains genetically similar to the fall-timed population that originally inhabited the river prior to these fisheries is unknown.

If the fall-timed chinook currently in the upper White River are not native to this river system, there is reason to be concerned about possible interbreeding between the native spring-run fish and these fall-run fish, if both groups of fish spawn at the same times and locations in the upper river.

The analysis of historical patterns of adult White River chinook arrivals at the Buckley trap and of catch indexes in the two relevant terminal area fisheries have been illuminating and they have caused us to modify our interpretations of the DNA results obtained in this investigation and our inferences about what the genetic data tell us about the effects of the White River Spring Chinook Recovery Program, the current stock status of chinook in the White River system, and the future of the White River spring-run chinook stock, as described in the Conclusions section below.

Other Factors

While we have not attempted to investigate the effects other factors have had on White River chinook runs, there is little doubt in our mind that these were likely substantial. Factors such as changes to in-stream flows resulting from the construction and operation of the Buckley Diversion and Mud Mountain Dams, extensive logging and other forms of habitat alteration in the basin, and other commercial and sport fisheries (both in the White and Puyallup Rivers and in Puget Sound and other marine waters) have all likely had major effects. Unfortunately, it may well be much more difficult or impossible to document and quantify the effects of these factors so our understanding of the whole system will likely continue to be incomplete. Nevertheless, we think it is important to recognize that other factors undoubtedly had significant effects on the nature and abundance of White River chinook runs.
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Conclusions

Taken together, we believe that the data and analyses presented above provide strong evidence supporting the following conclusions:

ì   The genetic characteristics (allele and genotype frequencies at microsatellite DNA, and allozyme, loci) of the chinook populations constituting the artificial production programs at the White River Hatchery and the Hupp Springs Hatchery were significantly different from those of the Voights Creek fall-run stock indicating that possible introgression of fall-run alleles into these stocks (if it has occurred) has been insufficient to convert the allele frequencies in the spring-run stocks to those typical of fall-run chinook.

Ù   The unmarked adult chinook arriving at the Buckley trap in1998 were of mixed spring-run and fall-run ancestry, based on their intermediate frequencies for many alleles, the observation that four microsatellite DNA loci were significantly (or nearly) out of Hardy Weinberg equilibrium in these fish, and on the stock-of-origin assignment analysis. Whether these fish were simply a mixture of only 'pure' spring-run fish and 'pure' fall-run fish or included some 'hybrid' spring-run x fall-run fish in addition is unknown.

Ú   The naturally produced smolts outmigrating from the White River in 2000 could have been produced by random interbreeding of adults, given the observation that all 14 microsatellite DNA loci screened in the smolt collection were in Hardy-Weinberg equilibrium. Because about 70% of these smolts were identified as spring-run and about 30% were identified as fall-run by the stock-of-origin analysis, there is some reason to be concerned about whether or not this is an indication of a significant level of interbreeding between the spring-run and fall-run stocks. While there is no compelling reason at present to conclude that inter-stock "hybridization" is a problem in the White River (see #5 below), the data and analyses presented in this report do not rule this out.

Û   There may have been important changes in the stock composition of the chinook salmon arriving at the Buckley trap over the past 45 years, as judged by the changing temporal patterns of arrival-timing. There were many years when only early-timed (= presumed spring-run) or predominantly late-timed (= presumed fall-run) fish were present and other periods when a mixture of run-timings was present. Whether or not the observed arrival-timing in past years was tightly correlated with genetic stock origin (spring-run vs. fall-run) is unknown for all of these years, but this seems to be a reasonable assumption given the pattern of stock-of-origin assignments observed for the adults in 1998 and the pattern of arrival timing in that year (Figures 4 and 5).

Ü   The tribal fishery in the lower White River may have harvested substantial numbers of White River chinook between 1944 and 1978 (based on estimates of catches) and it may have had important influences on both total abundance and the temporal pattern of adult arrivals at the Buckley trap. The effects of the tribal fishery in the lower Puyallup River on the White River chinook run are more difficult to document unambiguously, but have,

apparently, been substantial in at least some years. It seems likely from the timing and catch indexes of these fisheries that both spring-timed and fall-timed runs of chinook have existed in the lower White River since at least 1954, although hold-over and eventual late fishery harvest of spring-timed fish in the lower river could have caused the observed bi-phasic pattern of catches. It also seems clear that a spring-run was native to the upper White River; however, it is unclear whether an indigenous fall-timed stock existed in the upper White River. While impacts by these two tribal fisheries likely occurred, other fisheries (sport and commercial) in these two rivers, throughout Puget Sound, and in marine waters have, no doubt, also affected the abundance and characteristics of White River chinook.

Ý   We believe it is reasonable to conclude that the intentional removal of most of the spring-timed fish from the system to include them in the out-of-basin White River Spring Chinook Recovery Program (between 1977 and 1986) contributed to, and may have been largely responsible for, the virtual absence of a spring-timed chinook run to the upper White River (as inferred from the Buckley trap counts) from approximately 1978 through 1995. At the same time, we believe that the increased numbers and proportion of spring-timed fish seen since 1995 may be attributable to this recovery program.

These conclusions assume that: 1) the five collections analyzed in this study represented the populations from which they were taken; 2) there were not large year-to-year variations in genotype or allele frequencies in any of these populations; 3) all chinook stocks in the White River were included in our baseline; and 4) the counts of adult chinook at the Buckley trap and the estimates of tribal fisheries harvests, and the underlying species identification process, were reasonably accurate.

Unresolved Questions

Like many studies, the present investigation has uncovered previously unrecognized questions that hopefully will be answered by future investigations. Examples include:

1) What chinook stocks were native to the White River:
   1a) What stocks were present prior to 1900?
   1b) Was the spring-run chinook population in the White River in the 1950s native to the system?
   1c) Are the spring-run and fall-run chinook populations currently arriving at the Buckley trap genetically similar to, and descendants of, native White River stocks present in the system prior to 1954?

2) Why were fall-timed chinook so abundant in the upper White River runs in the years 1978 through 1995?

3) Is there a close association between observed time of adult arrival at the Buckley trap and genetic stock ancestry (e.g., are early arriving fish primarily spring-run stock genetically and late arriving fish primarily fall-run stock genetically?)? [The DNA stock-of-origin assignment results for the 1998 Buckley trap adult sample are consistent with the first generalization but not so with the second.]

4) What effects have the changed and variable in-stream flow regimes associated with dam construction and operation, negotiated minimum flow agreements, and or environmental changes in the basin had on the White River chinook?

5) Is there cause for concern regarding potential interbreeding between the spring-run population and the fall-timed population in the upper river:
   5a) Where in the upper river are spring-run and fall-run fish spawning?
   5b) When are the spring-run and fall-run fish spawning?
   5c) If spring-run and fall-run fish are spawning in the same places at the same times, is there any evidence of inter-stock hybrids?

6) What is happening in the lower White River:
   6a) What is the stock composition of the adults spawning in the lower White River?
   6b) Is there evidence that spawning of spring-run with fall-run fish in the lower river is producing inter-stock hybrids?

Recommended Future Genetic Analyses

In our minds, the single most significant limitation to the analysis we have done is that the genetic characterizations of the five populations of interest have been based on the analysis of only single-year's collections. For this reason, we strongly advocate the collection of additional samples from target populations and the DNA analysis of these collections and of a few already existing collections that have not yet been analyzed if there is a perceived need for additional genetic information about White River chinook.

Future Collections

We recommend the following specific field collections (of opercle punches or fin clips for DNA analysis):

1. Unmarked and untagged adults at the Buckley trap (N $200; sample every r^{th} fish throughout the return, where the sampling rate, r, is determined by the projected run size and adjusted, if necessary, in-season)

2. Outmigrating smolts from the upper White River (N $ 200; sampled every r^{th} fish throughout the outmigration, where r, the sampling rate, is determined by the expected number of outmigrants and adjusted, if necessary, in-season; not to include hatchery-origin smolts)

3. Spawning ground samples from specific upper White River localities:
   a) lower Clearwater River (up to 100 fish)
   b) lower Greenwater River (up to 100 fish)
   c) lower WF White River (up to 100 fish)
   d) lower Huckleberry Creek (up to 100 fish)

4. Spawning ground samples from lower White River localities (below Buckley Dam):
   a) Boise Creek (up to 100 fish)
   b) lower White River mainstem (up to 100 fish)

5. Adults from the Hupp Springs Hatchery (N = 100; sampled proportionately throughout the spawning period)

6. Adults from the White River Hatchery (N = 100; sampled proportionately throughout the spawning period)

7. Smolts from the lower White River (N = 100-200; sampled proportionately throughout the outmigration period; not to include hatchery-origin smolts)

Future DNA Analyses

We recommend the following specific genetic analyses:

1. DNA analysis of the new collections listed above
2. DNA analysis of existing upper White River spawning ground samples from 1995 (N=13), 1996 (N=68), & 1997 (N=21)
3. DNA analysis of the existing 1994 Hupp Springs & White River hatchery adult samples

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Table 1. Allele frequencies at 14 microsatellite DNA Loci in White River chinook.

One-8

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	156	0.000	0.000	0.006	0.017	0.012
2	160	0.065	0.077	0.097	0.112	0.077
3	162	0.009	0.000	0.000	0.006	0.000
4	164	0.028	0.011	0.028	0.034	0.018
5	166	0.000	0.000	0.000	0.006	0.000
6	168	0.028	0.011	0.034	0.028	0.012
7	170	0.287	0.187	0.165	0.101	0.018
8	172	0.176	0.253	0.222	0.129	0.250
9	174	0.102	0.143	0.108	0.163	0.119
10	176	0.157	0.159	0.170	0.191	0.214
11	178	0.046	0.033	0.063	0.107	0.101
12	182	0.028	0.022	0.006	0.034	0.107
13	184	0.000	0.005	0.006	0.000	0.024
14	186	0.074	0.099	0.097	0.073	0.048
# genes scored		108	182	176	178	168

Ots-1

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	184	0.000	0.005	0.000	0.000	0.000
2	188	0.217	0.190	0.339	0.381	0.494
3	190	0.017	0.022	0.017	0.000	0.000
4	192	0.400	0.446	0.278	0.290	0.229
5	194	0.050	0.065	0.061	0.028	0.012
6	196	0.317	0.272	0.306	0.295	0.265
7	198	0.000	0.000	0.000	0.006	0.000
# genes scored		120	184	180	176	166

Ots-108

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	100	0.095	0.110	0.129	0.159	0.153
2	108	0.016	0.023	0.062	0.023	0.091
3	112	0.159	0.122	0.140	0.199	0.136
4	116	0.008	0.017	0.000	0.006	0.011
5	120	0.000	0.006	0.000	0.006	0.000
6	124	0.294	0.349	0.236	0.205	0.267
7	128	0.000	0.006	0.022	0.011	0.034
8	132	0.143	0.093	0.202	0.153	0.170
9	144	0.000	0.000	0.000	0.011	0.011
10	152	0.000	0.012	0.011	0.000	0.000
11	164	0.000	0.000	0.006	0.000	0.000
12	168	0.000	0.000	0.000	0.011	0.011
13	172	0.151	0.134	0.129	0.108	0.057
14	180	0.000	0.006	0.000	0.000	0.023
15	184	0.071	0.041	0.028	0.057	0.017
16	188	0.024	0.035	0.006	0.017	0.000
17	192	0.016	0.012	0.011	0.006	0.011
18	200	0.016	0.000	0.000	0.000	0.000
19	204	0.008	0.035	0.017	0.028	0.000
20	220	0.000	0.000	0.000	0.000	0.006
# genes scored		126	172	178	176	176

Ots-3

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	62	0.000	0.005	0.000	0.000	0.000
2	78	0.000	0.000	0.010	0.000	0.022
3	84	0.000	0.000	0.005	0.005	0.000
4	86	0.056	0.057	0.082	0.071	0.070
5	88	0.000	0.000	0.000	0.005	0.000
6	90	0.056	0.031	0.098	0.087	0.188
7	92	0.648	0.620	0.603	0.643	0.441
8	94	0.077	0.047	0.067	0.056	0.081
9	96	0.162	0.240	0.134	0.122	0.172
10	98	0.000	0.000	0.000	0.005	0.016
11	100	0.000	0.000	0.000	0.005	0.011
# genes scored		142	192	194	196	186

[1] = allele size in base pairs

▨ = large difference in allele frequencies between spring and fall stocks

Table 1. (cont.) Allele frequencies at 14 microsatellite DNA Loci in White River chinook.

Ots-107

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	179	0.397	0.300	0.364	0.173	0.111
2	183	0.006	0.000	0.015	0.020	0.032
3	191	0.000	0.011	0.015	0.026	0.005
4	195	0.058	0.079	0.044	0.031	0.005
5	199	0.071	0.053	0.083	0.092	0.021
6	203	0.006	0.021	0.039	0.026	0.063
7	207	0.013	0.026	0.015	0.026	0.079
8	223	0.013	0.005	0.015	0.026	0.063
9	227	0.006	0.011	0.034	0.071	0.121
10	231	0.122	0.079	0.039	0.097	0.026
11	235	0.115	0.163	0.107	0.122	0.053
12	239	0.103	0.163	0.141	0.184	0.226
13	247	0.006	0.005	0.015	0.020	0.000
14	251	0.013	0.005	0.019	0.026	0.105
15	255	0.038	0.063	0.010	0.010	0.005
16	259	0.000	0.005	0.000	0.000	0.000
17	267	0.000	0.000	0.010	0.005	0.005
18	271	0.026	0.011	0.019	0.041	0.026
19	275	0.000	0.000	0.005	0.000	0.000
20	279	0.006	0.000	0.005	0.000	0.000
21	291	0.000	0.000	0.000	0.005	0.000
22	299	0.000	0.000	0.000	0.000	0.016
23	303	0.000	0.000	0.010	0.000	0.037
# genes scored		156	190	206	196	190

Ots-101

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	152	0.000	0.000	0.010	0.005	0.039
2	168	0.000	0.000	0.000	0.000	0.006
3	176	0.000	0.000	0.015	0.010	0.061
4	180	0.000	0.000	0.000	0.000	0.017
5	184	0.047	0.044	0.050	0.036	0.017
6	188	0.007	0.033	0.015	0.005	0.006
7	192	0.000	0.022	0.045	0.041	0.100
8	196	0.034	0.044	0.050	0.077	0.033
9	200	0.027	0.066	0.040	0.020	0.044
10	204	0.088	0.027	0.060	0.107	0.078
11	208	0.088	0.060	0.090	0.046	0.033
12	212	0.061	0.027	0.020	0.041	0.044
13	216	0.243	0.170	0.110	0.128	0.072
14	220	0.135	0.165	0.180	0.128	0.083
15	224	0.074	0.154	0.065	0.092	0.072
16	228	0.014	0.033	0.070	0.020	0.039
17	232	0.095	0.055	0.060	0.061	0.100
18	236	0.020	0.033	0.020	0.071	0.056
19	240	0.041	0.027	0.030	0.061	0.067
20	244	0.000	0.000	0.035	0.020	0.022
21	248	0.014	0.022	0.015	0.010	0.006
22	252	0.000	0.000	0.005	0.005	0.000
23	264	0.000	0.000	0.000	0.000	0.006
24	268	0.014	0.016	0.010	0.015	0.000
25	272	0.000	0.000	0.005	0.000	0.000
# genes scored		148	182	200	196	180

Ogo-2

alleles code	size[1]	White River Hatchery	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	216	0.013	0.006	0.006	0.008	0.007
2	218	0.025	0.083	0.056	0.077	0.007
3	220	0.075	0.019	0.074	0.023	0.021
4	222	0.000	0.006	0.000	0.015	0.007
5	224	0.425	0.449	0.444	0.469	0.667
6	226	0.250	0.212	0.247	0.169	0.194
7	228	0.025	0.006	0.012	0.008	0.021
8	230	0.025	0.006	0.025	0.038	0.007
9	232	0.025	0.000	0.006	0.062	0.014
10	234	0.038	0.032	0.012	0.031	0.021
11	238	0.075	0.167	0.117	0.077	0.035
12	240	0.025	0.013	0.000	0.023	0.000
# genes scored		80	156	162	130	144

Ocl-1

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	152	0.014	0.056	0.012	0.010	0.008
2	154	0.000	0.000	0.006	0.000	0.000
3	160	0.216	0.188	0.214	0.216	0.172
4	162	0.095	0.097	0.161	0.088	0.230
5	164	0.135	0.160	0.131	0.147	0.164
6	166	0.000	0.000	0.030	0.000	0.016
7	168	0.203	0.201	0.226	0.324	0.295
8	170	0.041	0.000	0.006	0.020	0.025
9	174	0.216	0.201	0.149	0.147	0.033
10	176	0.081	0.097	0.065	0.049	0.057
# genes scored		74	144	168	102	122

[1] = allele size in base pairs

▨ = large difference in allele frequencies between spring and fall stocks

Table 1. (cont.) Allele frequencies at 14 microsatellite DNA Loci in White River chinook.

Ots-2

alleles code	size[1]	White River Hatchery SP	Hupp Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	63	0.000	0.000	0.000	0.005	0.000
2	65	0.000	0.000	0.011	0.000	0.000
3	67	0.276	0.326	0.362	0.328	0.337
4	69	0.007	0.011	0.011	0.022	0.051
5	71	0.239	0.163	0.191	0.134	0.067
6	73	0.000	0.000	0.000	0.011	0.006
7	81	0.142	0.087	0.016	0.054	0.006
8	83	0.030	0.043	0.043	0.032	0.084
9	85	0.022	0.043	0.032	0.070	0.090
10	87	0.007	0.000	0.043	0.059	0.124
11	89	0.067	0.082	0.112	0.048	0.062
12	91	0.000	0.005	0.000	0.000	0.011
13	95	0.000	0.022	0.016	0.022	0.017
14	99	0.000	0.000	0.000	0.005	0.006
15	101	0.015	0.016	0.011	0.011	0.000
16	103	0.030	0.022	0.043	0.059	0.124
17	105	0.157	0.158	0.112	0.118	0.011
18	107	0.007	0.022	0.000	0.011	0.006
19	109	0.000	0.000	0.000	0.011	0.000
# genes scored		134	184	188	186	178

Ogo-4

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	131	0.000	0.000	0.000	coho	0.000
2	135	0.000	0.000	0.000	0.005	0.000
3	137	0.196	0.231	0.284	0.272	0.397
4	139	0.000	0.011	0.000	0.000	0.000
5	141	0.188	0.280	0.237	0.217	0.149
6	143	0.143	0.065	0.063	0.076	0.075
7	145	0.027	0.000	0.000	0.000	0.006
8	147	0.000	0.000	0.000	0.022	0.034
9	153	0.000	0.000	0.000	0.000	0.006
10	155	0.009	0.000	0.005	0.000	0.000
11	157	0.000	0.000	0.000	0.005	0.017
12	159	0.054	0.048	0.047	0.027	0.034
13	161	0.116	0.124	0.074	0.087	0.034
14	163	0.205	0.177	0.274	0.196	0.201
15	165	0.036	0.016	0.000	0.038	0.017
16	167	0.009	0.016	0.011	0.011	0.000
17	169	0.018	0.032	0.005	0.033	0.029
# genes scored		112	186	190	184	174

Str-73

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	123	0.092	0.088	0.057	0.063	0.021
2	125	0.000	0.000	0.000	0.000	0.010
3	127	0.112	0.060	0.063	0.078	0.010
4	129	0.122	0.137	0.108	0.104	0.036
5	135	0.010	0.000	0.006	0.000	0.000
6	137	0.000	0.033	0.040	0.042	0.094
7	139	0.286	0.203	0.313	0.229	0.313
8	141	0.184	0.247	0.205	0.208	0.307
9	145	0.092	0.104	0.125	0.151	0.104
10	147	0.010	0.005	0.006	0.016	0.031
11	149	0.020	0.060	0.045	0.026	0.052
12	155	0.000	0.000	0.000	0.021	0.021
13	157	0.031	0.049	0.011	0.042	0.000
14	159	0.000	0.000	0.006	0.010	0.000
15	177	0.041	0.011	0.017	0.010	0.000
# genes scored		98	182	176	192	192

Str-60

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	136	0.000	0.000	0.000	0.005	0.000
2	138	0.008	0.000	0.042	0.010	0.000
3	140	0.683	0.769	0.647	0.750	0.688
4	144	0.108	0.070	0.063	0.035	0.036
5	146	0.133	0.091	0.184	0.115	0.135
6	148	0.025	0.000	0.005	0.000	0.000
7	150	0.000	0.000	0.000	0.000	0.010
8	152	0.042	0.065	0.058	0.085	0.130
9	168	0.000	0.005	0.000	0.000	0.000
# genes scored		120	186	190	200	192

[1] = allele size in base pairs

▨ = large difference in allele frequencies between spring and fall stocks

Table 1. (cont.) Allele frequencies at 14 microsatellite DNA Loci in White River chinook.

Ots-104

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	176	0.000	0.011	0.023	0.005	0.000
2	180	0.028	0.005	0.028	0.010	0.027
3	184	0.028	0.000	0.017	0.000	0.005
4	188	0.000	0.000	0.000	0.000	0.005
5	200	0.000	0.000	0.006	0.000	0.000
6	204	0.056	0.048	0.040	0.026	0.027
7	208	0.028	0.011	0.023	0.031	0.005
8	212	0.292	0.204	0.165	0.209	0.043
9	216	0.160	0.183	0.136	0.143	0.071
10	220	0.035	0.038	0.051	0.041	0.082
11	224	0.021	0.011	0.023	0.051	0.092
12	228	0.056	0.075	0.114	0.097	0.136
13	232	0.000	0.022	0.040	0.031	0.071
14	240	0.000	0.005	0.040	0.031	0.060
15	244	0.000	0.032	0.017	0.015	0.038
16	248	0.125	0.108	0.051	0.092	0.054
17	252	0.000	0.027	0.000	0.020	0.011
18	256	0.049	0.075	0.051	0.015	0.005
19	260	0.021	0.011	0.011	0.010	0.054
20	264	0.083	0.097	0.108	0.051	0.033
21	268	0.000	0.011	0.023	0.036	0.071
22	272	0.021	0.016	0.011	0.020	0.043
23	276	0.000	0.000	0.000	0.015	0.011
24	280	0.000	0.000	0.000	0.005	0.005
25	284	0.000	0.005	0.000	0.010	0.016
26	288	0.000	0.000	0.000	0.005	0.005
27	292	0.000	0.005	0.017	0.031	0.027
28	296	0.000	0.000	0.006	0.000	0.000
# genes		144	186	176	196	184

Ssa-197

alleles code	size[1]	White River Hatchery SP	Hupp Springs Hatchery SP	White River unmarked adults	White River natural smolts	Voights Creek Hatchery Fall
1	112	0.000	0.000	0.000	coho	0.000
2	152	0.016	0.005	0.016	0.005	0.026
3	156	0.023	0.005	0.016	0.020	0.011
4	164	0.000	0.000	0.005	0.000	0.000
5	168	0.000	0.011	0.016	0.035	0.032
6	172	0.000	0.000	0.011	0.010	0.037
7	176	0.000	0.005	0.022	0.000	0.000
8	180	0.008	0.000	0.000	0.010	0.021
9	188	0.000	0.005	0.005	0.000	0.000
10	192	0.078	0.136	0.071	0.051	0.005
11	196	0.102	0.103	0.114	0.045	0.053
12	200	0.109	0.087	0.065	0.091	0.047
13	204	0.047	0.011	0.043	0.045	0.058
14	208	0.102	0.098	0.049	0.056	0.016
15	212	0.008	0.027	0.016	0.025	0.005
16	216	0.055	0.071	0.082	0.035	0.016
17	220	0.000	0.000	0.005	0.005	0.032
18	224	0.063	0.087	0.054	0.056	0.032
19	228	0.008	0.005	0.000	0.015	0.032
20	232	0.094	0.082	0.087	0.056	0.037
21	236	0.039	0.087	0.092	0.167	0.211
22	240	0.000	0.011	0.016	0.010	0.053
23	244	0.008	0.005	0.022	0.015	0.032
24	248	0.188	0.114	0.076	0.096	0.084
25	252	0.008	0.000	0.005	0.030	0.058
26	256	0.000	0.000	0.000	0.005	0.021
27	260	0.031	0.027	0.033	0.025	0.032
28	264	0.016	0.016	0.076	0.081	0.047
29	268	0.000	0.000	0.000	0.000	0.005
# genes scored		128	184	184	198	190

[1] = allele size in base pairs

▨ = large difference in allele frequencies between spring and fall stocks

Table 2. Hardy-Weinberg Test Results (using the Markov chain method; GENEPOP (Version 3.2a).

White River Hatchery spring-run adults			Hupp Springs Hatchery spring-run adults			Voights Creek Hatchery Fall-run adults			White River unmarked adults			White River natural smolts		
locus	p-val	S.E.	locus	p-val	S.E.	locus	P-val	S.E.	locus	p-val	S.E.	locus	p-val	S.E.
Ocl – 1	.6905	.0074	Ocl - 1	.9170	.0027	Ocl - 1	.3211	.0118	Ocl - 1	.5461	.0126	Ocl - 1	.1709	.0076
Ots – 101	**.0006**	**.0004**	Ots – 101	.6650	.0172	Ots – 101	.0255	.0072	Ots – 101	.1490	.0141	Ots – 101	.8382	.0139
Ots - 104	.0900	.0095	Ots - 104	.1024	.0129	Ots - 104	.0804	.0120	Ots - 104	.0208	.0047	Ots - 104	.5652	.0229
Ots – 2	.5246	.0165	Ots – 2	.2377	.0140	Ots – 2	.2988	.0181	Ots – 2	.4473	.0172	Ots – 2	.0585	.0091
Ots – 3	.6716	.0056	**Ots – 3**	**.0007**	**.0003**	Ots – 3	.1836	.0090	Ots – 3	.1286	.0073	Ots – 3	.4268	.0160
Ogo – 2	.1972	.0146	Ogo – 2	.0674	.0084	Ogo – 2	.0292	.0068	Ogo – 2	.8591	.0092	Ogo – 2	.4526	.0179
Ogo – 4	.0571	.0060	Ogo – 4	.0823	.0079	Ogo – 4	.4272	.0170	Ogo – 4	.0039	.0010	Ogo – 4	.3025	.0156
One – 8	.0911	.0076	One – 8	.3454	.0134	One – 8	.1410	.0096	One – 8	.4203	.0142	One – 8	.7796	.0110
Ots – 1	.0890	.0038	Ots – 1	.0288	.0024	Ots – 1	.1751		Ots – 1	.2849	.0063	Ots – 1	.7000	.0062
Ots – 107	.0097	.0038	Ots – 107	.0335	.0067	Ots – 107	.4746	.0196	**Ots – 107**	**.0030**	**.0016**	Ots – 107	.0484	.0069
Ots – 108	.3058	.0157	Ots – 108	.3676	.0183	Ots – 108	.3498	.0177	Ots – 108	.1661	.0126	Ots – 108	.2500	.0166
Ssa – 197	.1349	.0144	Ssa – 197	.0539	.0088	Ssa – 197	.3593	.0224	Ssa – 197	.0078	.0043	Ssa – 197	.1237	.0151
Str – 60	**.0000**	**.0000**	Str – 60	.3245	.0076	Str – 60	.6200	.0072	**Str – 60**	**.0000**	**.0000**	Str – 60	.1949	.0087
Str - 73	.7268	.0119	Str - 73	.9532	.0037	Str - 73	.8106	.0119	Str - 73	.8151	.0124	Str - 73	.4493	.0153

Underlined Values = unadjusted P<0.01
Bold Underlined Values = test result significant after adjustment for multiple tests (P < 0.05/14 tests; = 0.0036)

Table 3. Results of tests of genic differentiation for each populations pair (using GENEPOP vers. 3.2a).

P-value for each population pair across all loci (Fisher's method)

Population Pair		$\chi 2$	df	Unadjusted P-value	P-value after adjustment for 10 tests
White River unmarked adults &	White River natural smolts	68.191	28	0.00003	0.0003
White River unmarked adults &	White River Hatchery SP	85.917	28	0.00000	0.0000
White River unmarked adults &	Hupp Springs Hatchery SP	102.921	28	0.00000	0.0000
White River unmarked adults &	Voights Cr Hatchery FALL	Infinity	28	<<0.00000	<0.0000
White River natural smolts &	White River Hatchery SP	Infinity	28	<<0.00000	<0.0000
White River natural smolts &	Hupp Springs Hatchery SP	Infinity	28	<<0.00000	<0.0000
White River natural smolts &	Voights Cr Hatchery FALL	Infinity	28	<<0.00000	<0.0000
White River Hatchery SP &	Hupp Springs Hatchery SP	47.895	28	0.01100	0.1100
White River Hatchery SP &	Voights Cr Hatchery FALL	Infinity	28	<<0.00000	<0.0000
Hupp Springs Hatchery SP &	Voights Cr Hatchery FALL	Infinity	28	<<0.00000	<0.0000

Table 4. Results of Pairwise Tests of Genotypic Differentiation (using GENEPOP vers. 3.2a) (tabulated P-values not adjusted for multiple tests).

Hupp Springs Hatchery SP (98CP) vs. Voights Creek Hatchery F (98CQ)

Locus	P-value	S.E.
Ocl-1	0.0000	0.0000
Ots-101	0.0000	0.0000
Ots-104	0.0000	0.0000
Ots-2	0.0000	0.0000
Ots-3	0.0000	0.0000
Ogo-2	0.0002	0.0001
Ogo-4	0.0000	0.0000
One-8	0.0000	0.0000
Ots-1	0.0000	0.0000
Ots-107	0.0000	0.0000
Ots-108	0.0000	0.0000
Ssa-197	0.0000	0.0000
Str-60	0.0229	0.0018
Str-73	0.0000	0.0000
All	0.0000	$P^2_{28} = 4$

White River Hatchery SP (98CO) vs. Hupp Springs Hatchery SP (98CP)

Locus	P-value	S.E.
Ocl-1	0.2393	0.0048
Ots-101	0.0308	0.0021
Ots-104	0.0130	0.0012
Ots-2	0.4160	0.0069
Ots-3	0.3754	0.0065
Ogo-2	0.1081	0.0037
Ogo-4	0.0853	0.0035
One-8	0.5322	0.0066
Ots-1	0.9172	0.0021
Ots-107	0.4407	0.0073
Ots-108	0.5965	0.0066
Ssa-197	0.4706	0.0079
Str-60	0.1257	0.0038
Str-73	0.1012	0.0039
All	0.0177	$P^2_{28} = 45.9$

White River natural smolts (00BE) vs. White River Hatchery SP (98CP)

Locus	P-value	S.E.
Ocl-1	0.7303	0.0041
Ots-101	0.0155	0.0015
Ots-104	0.0002	0.0001
Ots-2	0.0059	0.0007
Ots-3	0.7897	0.0052
Ogo-2	0.5380	0.0060
Ogo-4	0.1888	0.0052
One-8	0.0223	0.0017
Ots-1	0.0191	0.0012
Ots-107	0.0000	0.0000
Ots-108	0.3768	0.0067
Ssa-197	0.0046	0.0008
Str-60	0.0570	0.0025
Str-73	0.0973	0.0035
All	0.0000	$P^2_{28} = 105.7$

White River Hatchery SP (98CO) vs. Voights Creek Hatchery F (98CQ)

Locus	P-value	S.E.
Ocl-1	0.0019	0.0003
Ots-101	0.0000	0.0000
Ots-104	0.0000	0.0000
Ots-2	0.0000	0.0000
Ots-3	0.0004	0.0001
Ogo-2	0.1173	0.0033
Ogo-4	0.0003	0.0001
One-8	0.0000	0.0000
Ots-1	0.0000	0.0000
Ots-107	0.0000	0.0000
Ots-108	0.0000	0.0000
Ssa-197	0.0000	0.0000
Str-60	0.0033	0.0004
Str-73	0.0000	0.0000
All	0.0000	$P^2_{28} = 4$

White River natural smolts (00BE) vs. Voights Creek Hatchery F (98CQ)

Locus	P-value	S.E.
Ocl-1	0.0248	0.0014
Ots-101	0.0110	0.0015
Ots-104	0.0000	0.0000
Ots-2	0.0000	0.0000
Ots-3	0.0014	0.0003
Ogo-2	0.0034	0.0005
Ogo-4	0.1379	0.0047
One-8	0.0004	0.0002
Ots-1	0.1651	0.0044
Ots-107	0.0000	0.0000
Ots-108	0.0022	0.0004
Ssa-197	0.0034	0.0006
Str-60	0.3168	0.0068
Str-73	0.0000	0.0000
All	0.0000	$P^2_{28} = 4$

White River natural smolts (00BE) vs. Hupp Springs Hatchery SP (98CP)

Locus	P-value	S.E.
Ocl-1	0.0522	0.0023
Ots-101	0.0018	0.0003
Ots-104	0.0285	0.0023
Ots-2	0.0109	0.0012
Ots-3	0.0124	0.0013
Ogo-2	0.0338	0.0021
Ogo-4	0.2168	0.0059
One-8	0.0021	0.0005
Ots-1	0.0001	0.0001
Ots-107	0.0001	0.0001
Ots-108	0.0785	0.0039
Ssa-197	0.0001	0.0001
Str-60	0.3478	0.0078
Str-73	0.2523	0.0065
All	0.0000	$P^2_{28} = 130.8$

Table 4. (cont.) Results of Pairwise tests of genotypic differentiation (using GENEPOP vers. 3.2a) (tabulated P-values not adjusted for multiple tests).

White River unmarked adults (98CB) vs.
White River Hatchery SP (98CO)

Locus	P-value	S.E.
Ocl-1	0.3710	0.0052
Ots-101	0.0013	0.0003
Ots-104	0.0006	0.0002
Ots-2	0.0008	0.0002
Ots-3	0.4670	0.0062
Ogo-2	0.6279	0.0059
Ogo-4	0.0123	0.0011
One-8	0.5356	0.0072
Ots-1	0.2878	0.0040
Ots-107	0.1065	0.0039
Ots-108	0.0898	0.0036
Ssa-197	0.0571	0.0033
Str-60	0.3063	0.0052
Str-73	0.3618	0.0066
All	0.0000	$P^2_{28} = 78.7$

White River unmarked adults (98CB) vs.
Voights Creek Hatchery F (98CQ)

Locus	P-value	S.E.
Ocl-1	0.0550	0.0023
Ots-101	0.0010	0.0003
Ots-104	0.0000	0.0000
Ots-2	0.0000	0.0000
Ots-3	0.0126	0.0011
Ogo-2	0.0019	0.0003
Ogo-4	0.0002	0.0001
One-8	0.0000	0.0000
Ots-1	0.0051	0.0007
Ots-107	0.0000	0.0000
Ots-108	0.0326	0.0023
Ssa-197	0.0000	0.0000
Str-60	0.0041	0.0005
Str-73	0.0000	0.0000
All	0.0000	$P^2_{28} = 4$

White River unmarked adults (98CB) vs.
Hupp Springs Hatchery SP (98CP)

Locus	P-value	S.E.
Ocl-1	0.0321	0.0018
Ots-101	0.0209	0.0019
Ots-104	0.0649	0.0035
Ots-2	0.0033	0.0005
Ots-3	0.0061	0.0007
Ogo-2	0.1817	0.0055
Ogo-4	0.0438	0.0027
One-8	0.6651	0.0069
Ots-1	0.0130	0.0010
Ots-107	0.0164	0.0014
Ots-108	0.0244	0.0017
Ssa-197	0.1241	0.0054
Str-60	0.0068	0.0007
Str-73	0.3291	0.0068
All	0.0000	$P^2_{28} = 92.9$

White River unmarked adults (98CB) vs.
White River natural smolts (00BE)

Locus	P-value	S.E.
Ocl-1	0.3069	0.0054
Ots-101	0.1639	0.0060
Ots-104	0.0706	0.0040
Ots-2	0.0886	0.0040
Ots-3	0.8387	0.0036
Ogo-2	0.0173	0.0015
Ogo-4	0.0135	0.0013
One-8	0.1179	0.0047
Ots-1	0.2822	0.0050
Ots-107	0.0455	0.0027
Ots-108	0.2102	0.0056
Ssa-197	0.1059	0.0049
Str-60	0.0859	0.0030
Str-73	0.3907	0.0073
All	0.0003	$P^2_{28} = 60.6$

Table 5. Summary of WHICHRUN stock-of-origin assignments for unmarked adult chinook returning to the Buckley trap on the White River in 1998 using a three-stock baseline.

WRH sp = White River Hatchery spring-run
HSH sp = Hupp Springs Hatchery spring-run
VCH f = Voights Creek Hatchery fall-run
☐ = fewer than 9 loci scored
   * = fish had one or more alleles not observed in any baseline population

fish ID	date	most likely stock	# loci scored	fish ID	date	most likely stock	# loci scored
98CB 1	8-Jul	WRH sp	14	98CB 54	21-Aug	WRH sp	14
98CB 2	8-Jul	HSH sp	14	98CB 55	24-Aug	HSH sp	12
98CB 3	10-Jul	WRH sp	13	98CB 56	24-Aug	WRH sp	12
98CB 4	10-Jul	WRH sp	13	98CB 57	24-Aug	WRH sp	14
98CB 5	10-Jul	HSH sp	11	98CB 58	24-Aug	HSH sp	14
98CB 6	10-Jul	WRH sp	14	98CB 59	26-Aug	WRH sp	14
98CB 7	13-Jul	WRH sp	14	98CB 60	28-Aug	WRH sp	7
98CB 8	13-Jul	WRH sp	14	98CB 61	28-Aug	VCH f	13
98CB 9	13-Jul	WRH sp	13	98CB 62*	28-Aug	WRH sp	14
98CB 10	15-Jul	WRH sp	14	98CB 63	28-Aug	HSH sp	14
98CB 11	17-Jul	HSH sp	12	98CB 64	8-Sep	HSH sp	14
98CB 12*	17-Jul	WRH sp	14	98CB 65	8-Sep	VCH f	13
98CB 13	20-Jul	HSH sp	14	98CB 66	9-Sep	HSH sp	14
98CB 14	20-Jul	WRH sp	13	98CB 67	9-Sep	HSH sp	14
98CB 15	20-Jul	HSH sp	3	98CB 68	11-Sep	VCH f	14
98CB 16	20-Jul	HSH sp	12	98CB 69	11-Sep	VCH f	9
98CB 17	22-Jul	WRH sp	14	98CB 70*	11-Sep	VCH f	13
98CB 18	22-Jul	HSH sp	12	98CB 71	11-Sep	WRH sp	14
98CB 19	22-Jul	HSH sp	14	98CB 72	11-Sep	WRH sp	14
98CB 20	22-Jul	HSH sp	13	98CB 73	14-Sep	VCH f	14
98CB 21	22-Jul	WRH sp	14	98CB 74	14-Sep	VCH f	14
98CB 22	24-Jul	WRH sp	14	98CB 75	14-Sep	WRH sp	14
98CB 23	24-Jul	HSH sp	2	98CB 76	14-Sep	VCH f	14
98CB 24	24-Jul		0	98CB 77	15-Sep	WRH sp	13
98CB 25	24-Jul	WRH sp	14	98CB 78	15-Sep	WRH sp	13
98CB 26	27-Jul	WRH sp	12	98CB 79	16-Sep	WRH sp	14
98CB 27	27-Jul	HSH sp	12	98CB 80	16-Sep	HSH sp	14
98CB 28	29-Jul	WRH sp	11	98CB 81	21-Sep	VCH f	14
98CB 29	31-Jul	WRH sp	7	98CB 82	21-Sep	VCH f	14
98CB 30	3-Aug	WRH sp	14	98CB 83	21-Sep	VCH f	9
98CB 31	3-Aug	HSH sp	14	98CB 84	21-Sep	VCH f	12
98CB 32	3-Aug	WRH sp	9	98CB 85	21-Sep	WRH sp	13
98CB 33	5-Aug	WRH sp	14	98CB 86*	21-Sep	VCH f	14
98CB 34	5-Aug	WRH sp	14	98CB 87	21-Sep	VCH f	13
98CB 35	5-Aug	VCH f	10	98CB 88	21-Sep	VCH f	14
98CB 36*	7-Aug	HSH sp	13	98CB 89	21-Sep	VCH f	12
98CB 37	10-Aug	HSH sp	14	98CB 90	21-Sep	VCH f	11
98CB 38*	14-Aug	HSH sp	6	98CB 91	22-Sep	VCH f	6
98CB 39	17-Aug	WRH sp	14	98CB 92	22-Sep	VCH f	13
98CB 40	17-Aug	WRH sp	3	98CB 93	23-Sep	VCH f	7
98CB 41	17-Aug	HSH sp	13	98CB 94	23-Sep	VCH f	7
98CB 42	19-Aug	WRH sp	14	98CB 95	25-Sep	VCH f	4
98CB 43	19-Aug	WRH sp	5	98CB 96	24-Sep	VCH f	14
98CB 44	19-Aug	HSH sp	13	98CB 97	28-Sep	WRH sp	14
98CB 45	19-Aug	WRH sp	14	98CB 98	28-Sep	VCH f	14
98CB 46*	19-Aug	VCH f	13	98CB 99	30-Sep	WRH sp	13
98CB 47	19-Aug	HSH sp	14	98CB 100	2-Oct	HSH sp	14
98CB 48	19-Aug	WRH sp	6	98CB 101*	5-Oct	VCH f	14
98CB 49	19-Aug	HSH sp	14	98CB 102	7-Oct	VCH f	14
98CB 50	19-Aug	VCH f	14	98CB 103	7-Oct	HSH sp	11
98CB 51	19-Aug	WRH sp	14	98CB 104	9-Oct	VCH f	14
98CB 52*	21-Aug	HSH sp	14	98CB 105	13-Oct	VCH f	14
98CB 53	21-Aug	HSH sp	14				

Table 6. Results of three simulation analyses where all simulated fish came from one of the three baseline populations. (Note that independent resampling was done for generating the baseline fish and the unknown mixture fish in each iteration.)

100% of the simulated fish from the White River Hatchery spring-run population

	WHICHRUN Estimate		Adjusted Estimate	
	estimate	se	estimate	se
White River Hatchery (SP)	84.5%	(± 4.8)	98.6%	(± 2.9)
Hupp Springs Hatchery (SP)	14.8%	(± 4.8)	1.4%	(± 2.9)
Voights Creek Hatchery (F)	0.6%	(± 0.7)	0.1%	(± 0.2)

100% of the simulated fish from the Hupp Springs Hatchery spring-run population

	WHICHRUN Estimate		Adjusted Estimate	
	estimate	se	estimate	se
White River Hatchery (SP)	25.8%	(± 6.2)	8.4%	(± 7.7)
Hupp Springs Hatchery (SP)	73.4%	(± 6.3)	91.5%	(± 7.7)
Voights Creek Hatchery (F)	0.9%	(± 0.9)	0.1%	(± 0.3)

100% of the simulated fish from the Voights Creek Hatchery fall-run population

	WHICHRUN Estimate		Adjusted Estimate	
	estimate	se	estimate	se
White River Hatchery (SP)	0.9%	(± 1.4)	0.1%	(± 0.4)
Hupp Springs Hatchery (SP)	1.7%	(± 1.4)	0.2%	(± 0.5)
Voights Creek Hatchery (F)	97.5%	(± 1.8)	99.7%	(± 0.6)

Table 7. Summary of arrival timing at Buckley trap (1954-2000).

Values indicate % of run observed in each of three time periods (jacks as a % of total run also tabulated)

Year	total N	% jacks	before weekending including July 1	after 2nd week of Aug	after weekending including Sept. 30
1954	633	nd	35.7%	10.6%	3.318%
1955	632	nd	32.0%	2.8%	0.8%
1956	794	nd	51.6%	4.2%	0.3%
1957	374	nd	78.3%	6.4%	0.3%
1958	245	nd	73.9%	5.7%	0.0%
1959	261	nd	30.3%	23.8%	1.5%
1960	528	nd	82.8%	3.8%	3.2%
1961	505	nd	59.6%	4.8%	1.8%
1962	164	nd	79.3%	7.3%	0.6%
1963	447	nd	74.0%	5.8%	0.2%
1964	658	nd	58.8%	3.8%	0.0%
1965	969	nd	77.0%	1.2%	0.0%
1966	639	nd	38.3%	2.8%	0.0%
1967	654	nd	51.1%	4.0%	0.6%
1968	417	nd	64.0%	8.4%	0.0%
1969	534	nd	74.7%	4.1%	0.0%
1970	555	nd	65.8%	4.3%	0.0%
1971	393	nd	23.9%	3.8%	0.0%
1972	392	nd	31.9%	12.0%	1.0%
1973	137	nd	12.4%	59.9%	15.3%
1974	388	nd	26.0%	12.4%	0.8%
1975	794	nd	15.8%	37.1%	0.0%
1976	229	3.5%	32.3%	10.5%	0.0%
1977	66	33.3%	57.6%	15.2%	0.0%
1978	140	37.1%	8.6%	82.1%	2.1%
1979	72	20.8%	38.9%	9.7%	0.0%
1980	61	6.6%	52.5%	23.0%	0.0%
1981	199	10.6%	7.0%	87.4%	59.3%
1982	20	15.0%	0.0%	35.0%	15.0%
1983	26	19.2%	23.1%	7.7%	0.0%
1984	10	30.0%	10.0%	30.0%	0.0%
1985	24	0.0%	0.0%	100.0%	41.7%
1986	8	25.0%	12.5%	87.5%	0.0%
1987	117	0.0%	0.9%	99.1%	49.6%
1988	129	1.6%	5.4%	91.5%	10.1%
1989	111	0.0%	6.3%	69.4%	21.6%
1990	275	0.0%	8.0%	80.4%	6.2%
1991	290	32.8%	1.0%	95.9%	8.3%
1992	424	4.0%	1.2%	89.4%	9.0%
1993	419	3.6%	0.0%	92.1%	21.2%
1994	571	31.5%	1.6%	91.2%	18.0%
1995	813	25.6%	0.0%	80.0%	11.4%
1996	715	13.4%	4.9%	59.3%	4.3%
1997	494	18.6%	1.0%	46.0%	1.2%
1998	402	20.4%	11.2%	51.2%	3.7%
1999	1,292	57.2%	1.2%	41.9%	1.7%
2000	1,546	1.5%	13.2%	41.1%	5.1%

(Years 1977-1986 marked as "Recovery Program")

key:	> 30%	< 10%	< 3.32%
	intermediate	*intermediate*	*intermediate*
	<10%	**>25%**	**> 8%**

nd = no data (no jacks appear in USACE records until 1976 counts)
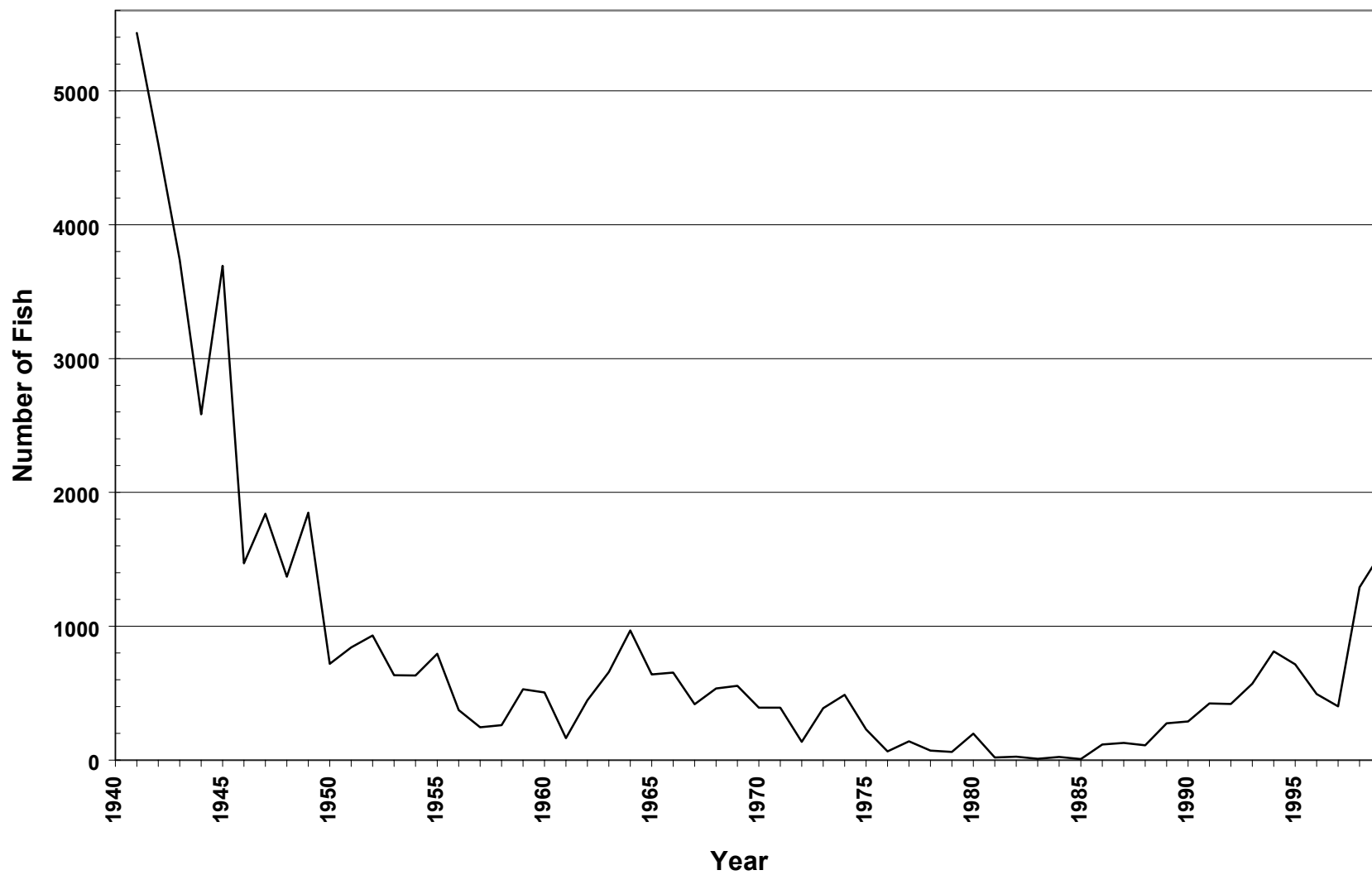
Figure 1. Annual chinook arrivals at the Buckley trap on the Upper White River (see Appendix Table 4 for actual counts).
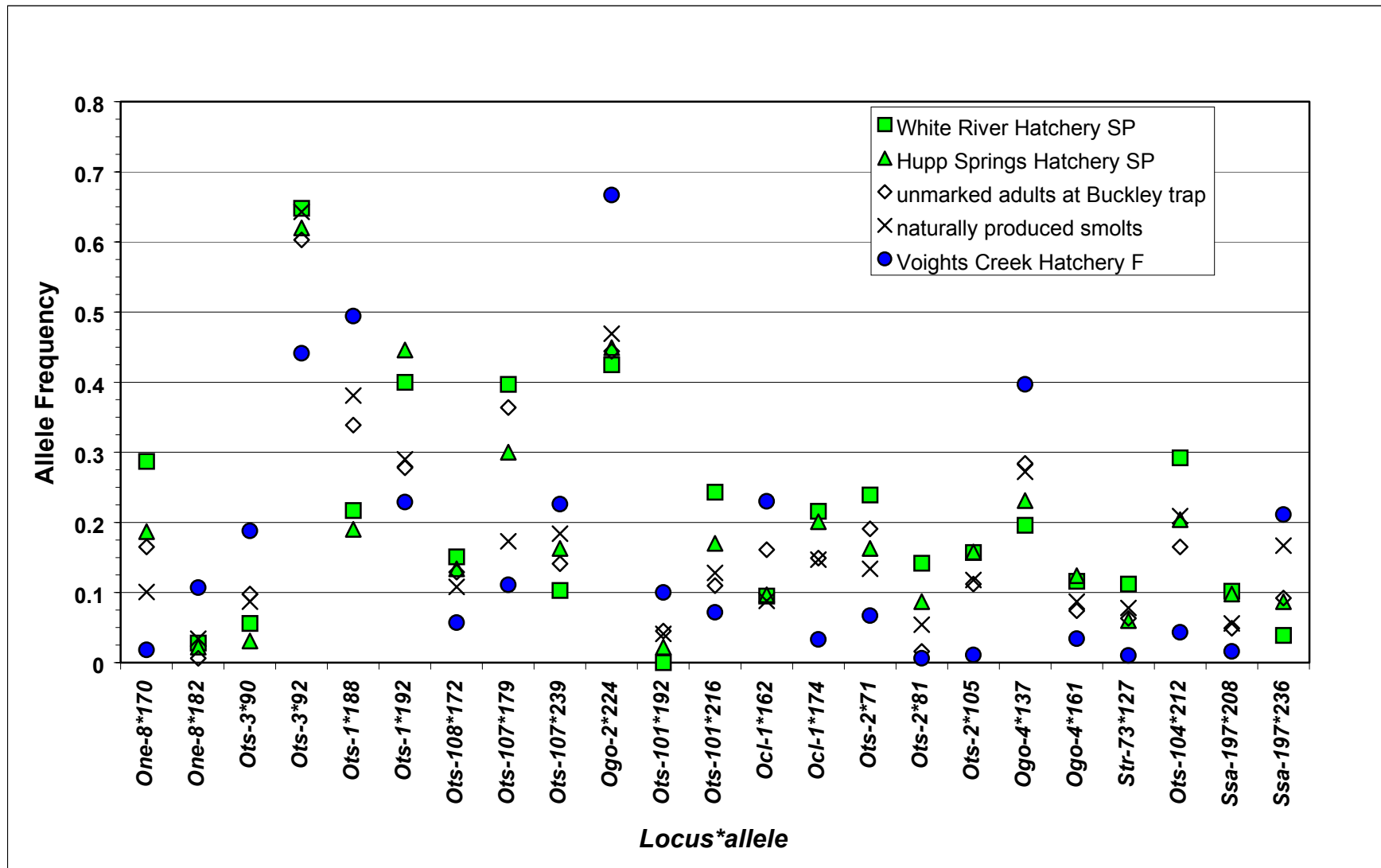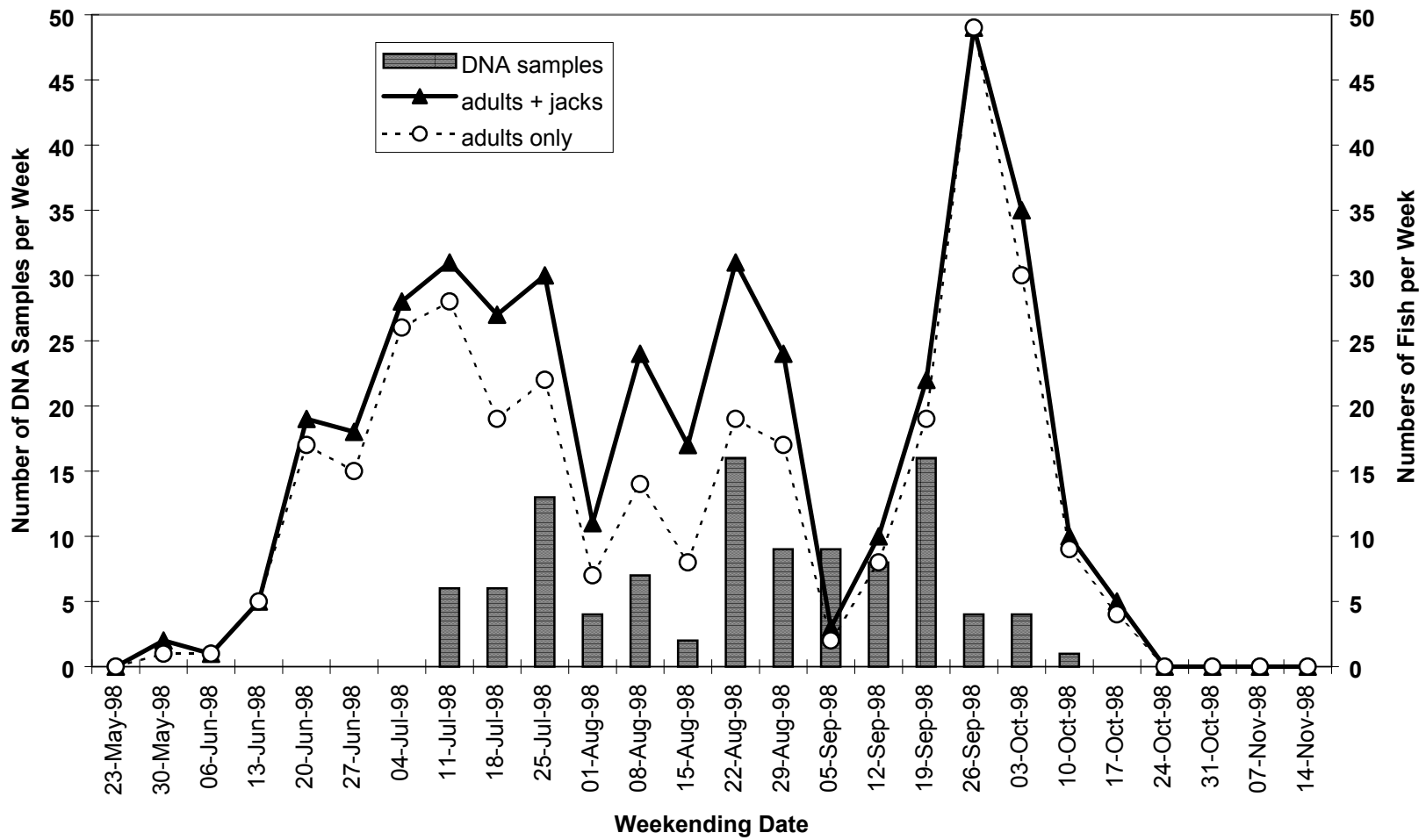
Figure 2. Frequency variation at 23 selected microsatellite DNA alleles in the five chinook collections.
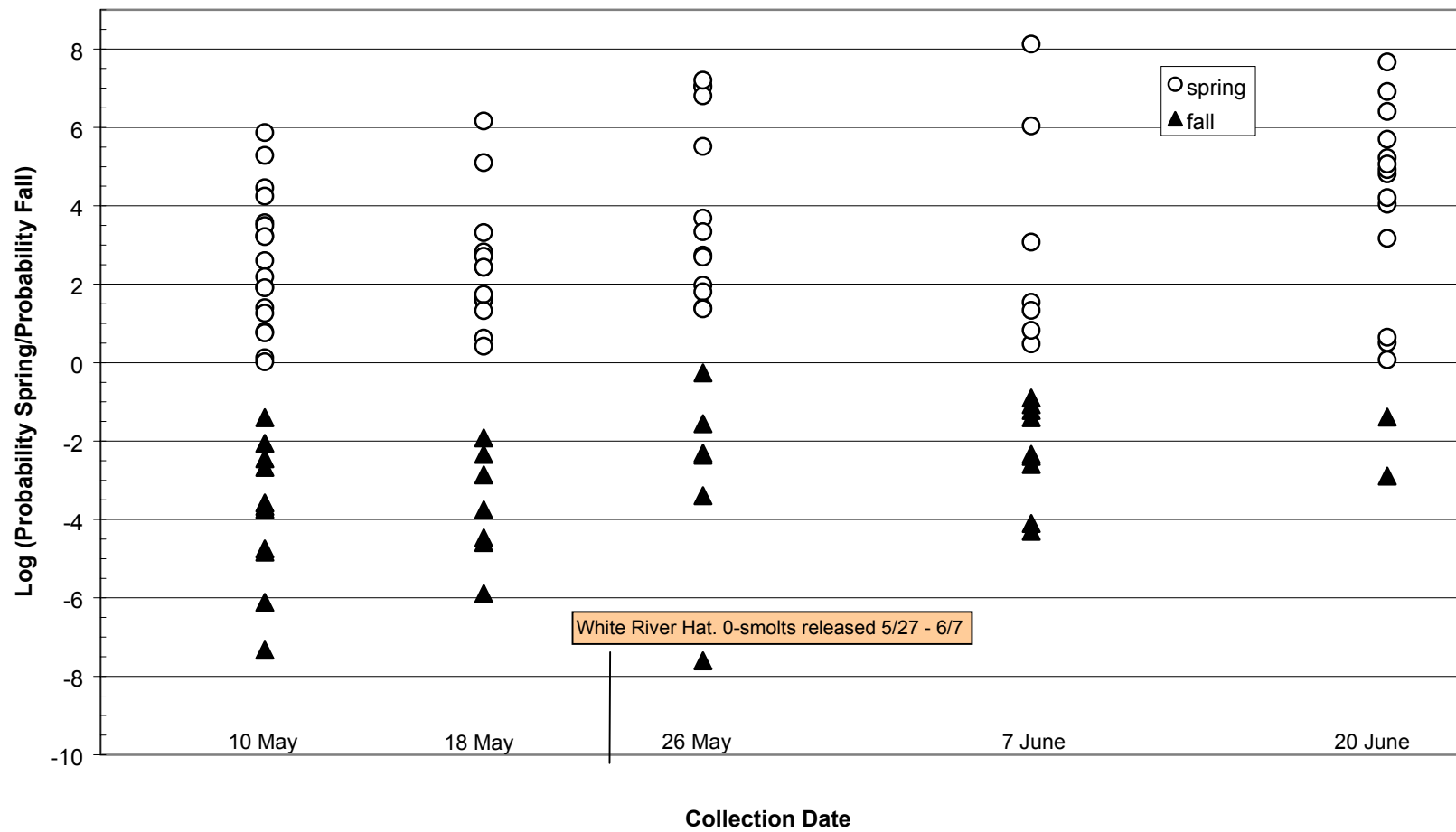
Figure 3. DNA stock-of-origin assignments (using WHICHRUN) for smolts collected in 2000 (N=100).
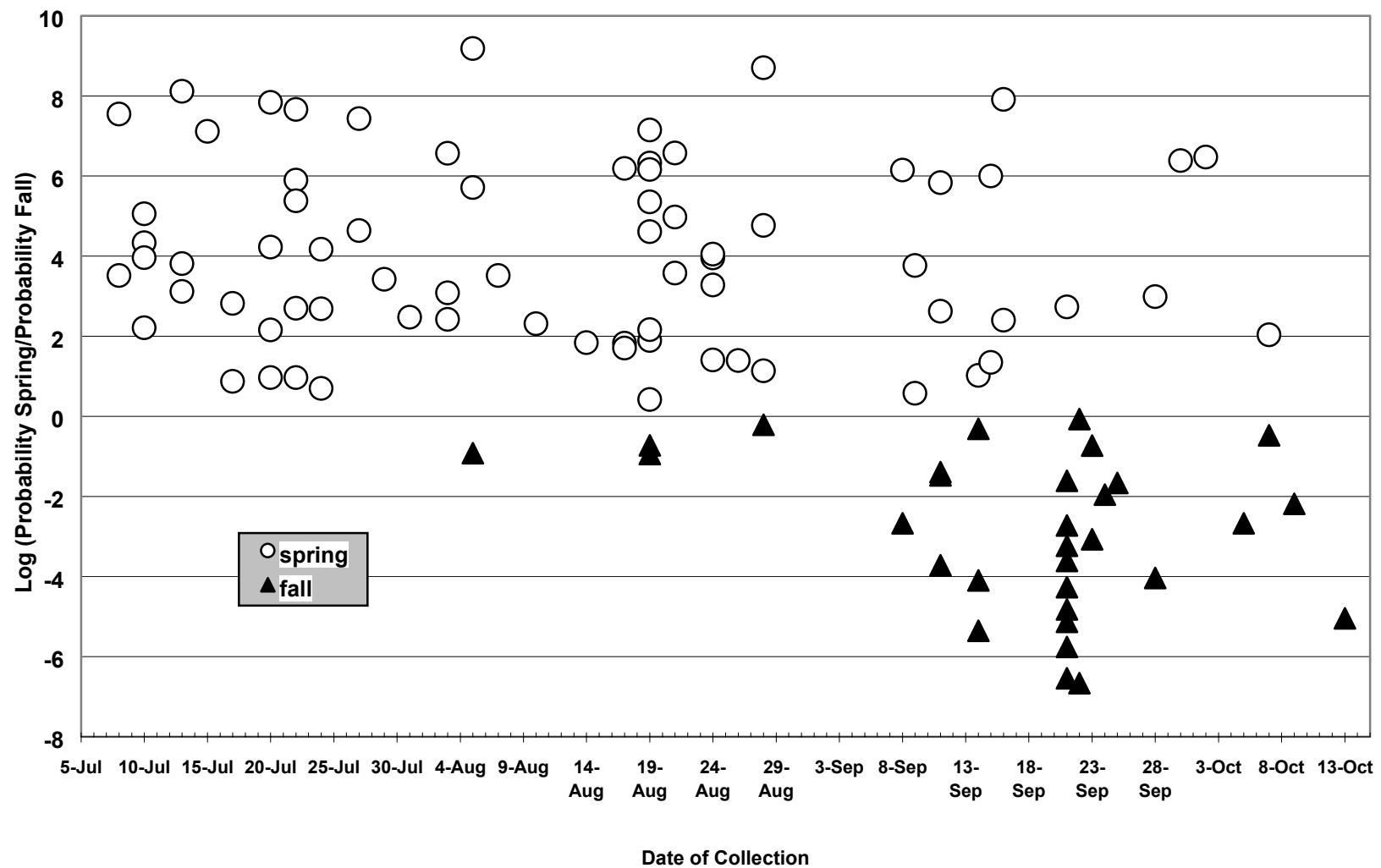
Figure 4. Adjusted DNA stock-of-origin assignments for 1998 Buckley trap adult chinook (N=104).

Figure 5. Relationship between DNA sampling and chinook arrivals at the Buckley trap in 1998.
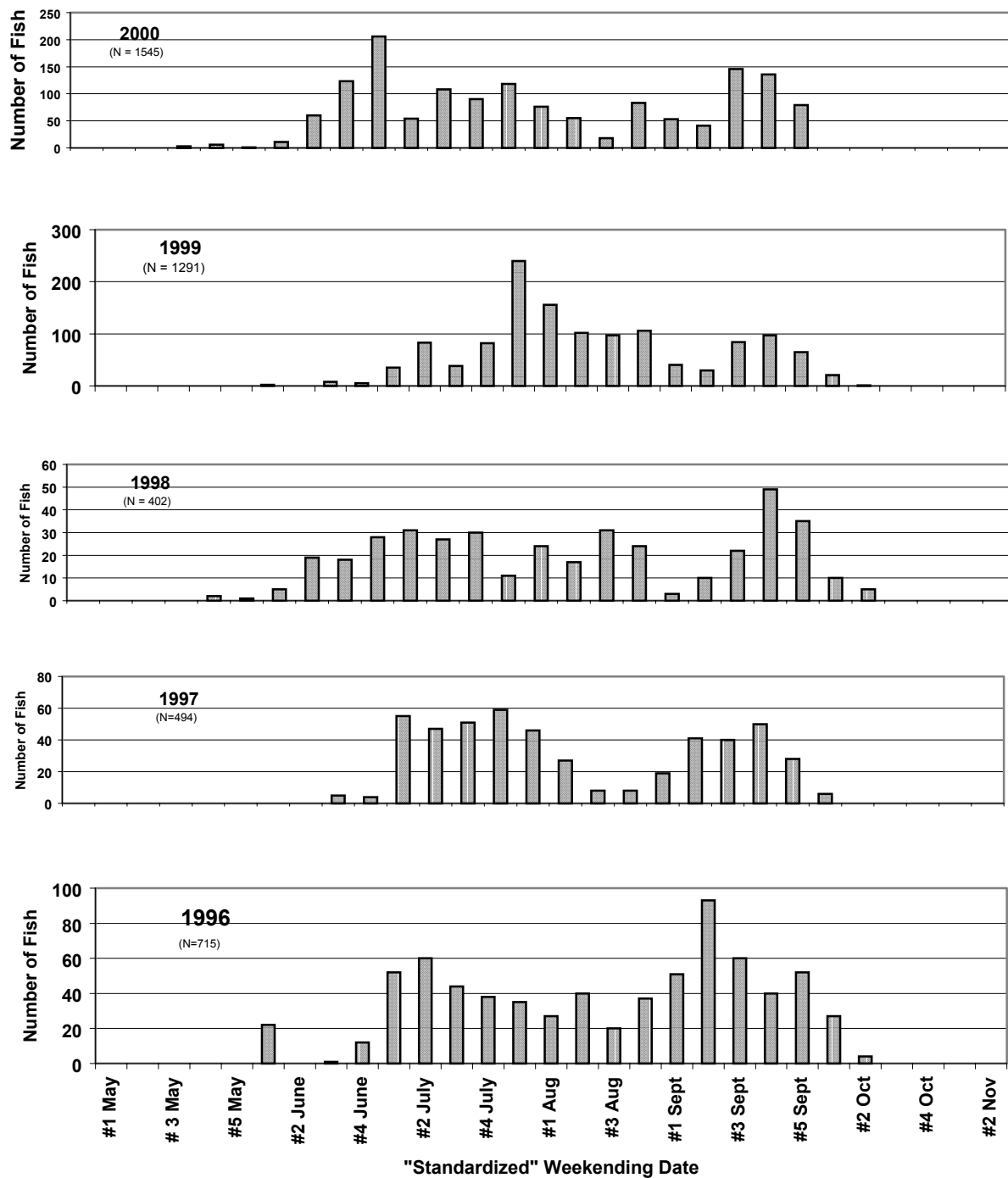
Figure 6. Patterns of chinook arrival timing at Buckley trap, 1996-2000.
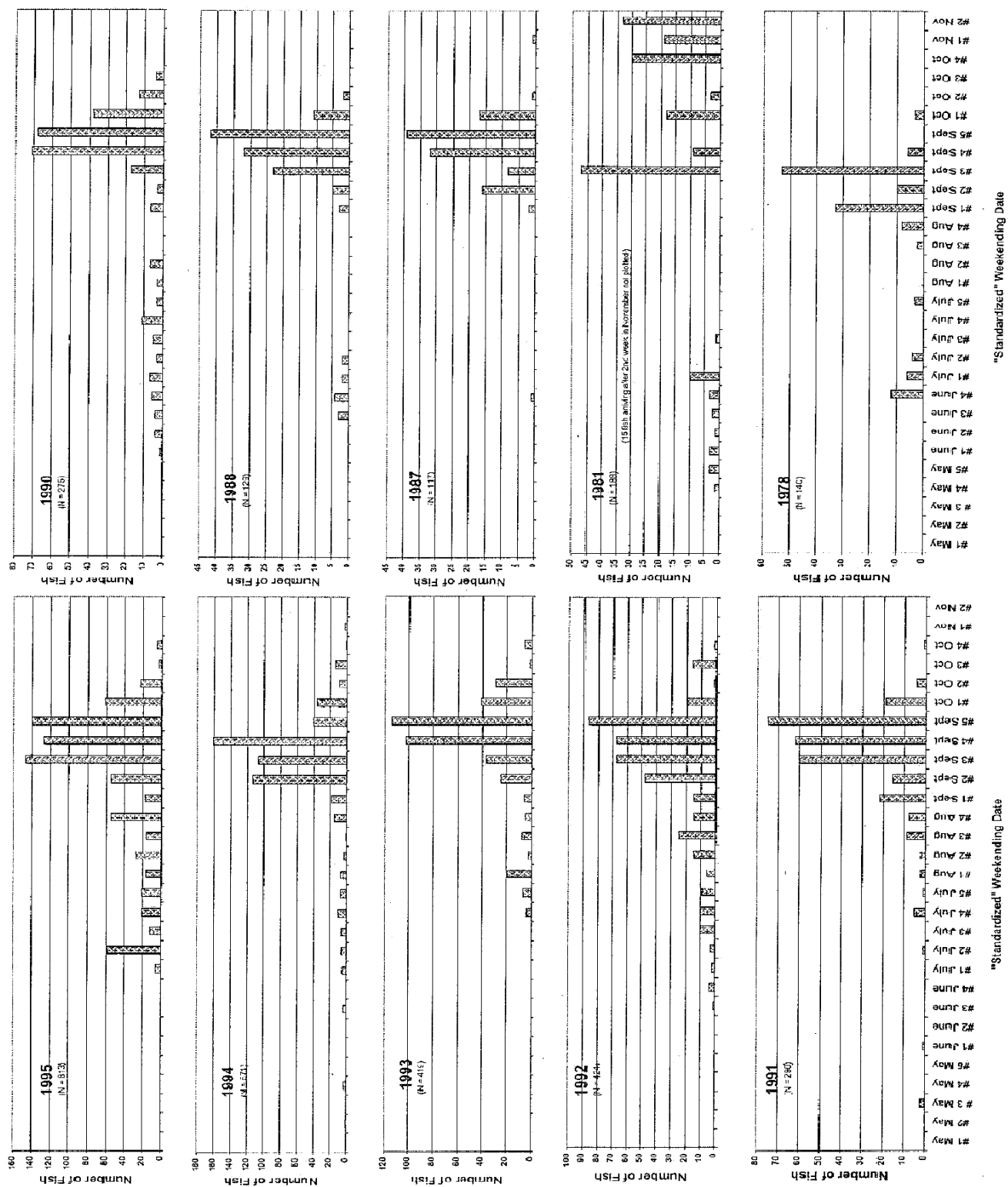
Figure 7. Patterns of chinook arrival timing at Buckley trap, 1995-1978.
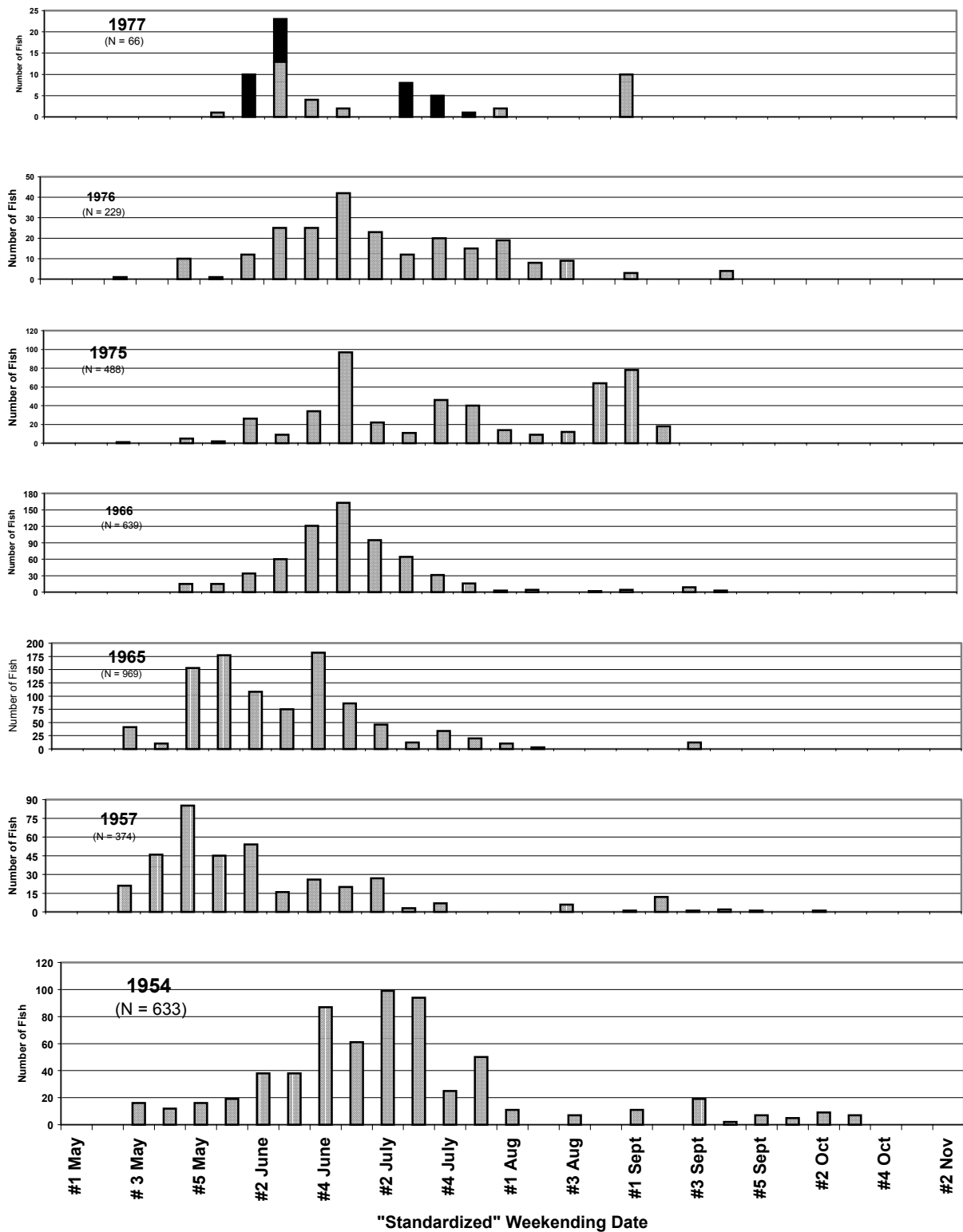
Figure 8. Patterns of chinook arrival timing at Buckley trap, 1954-1977.
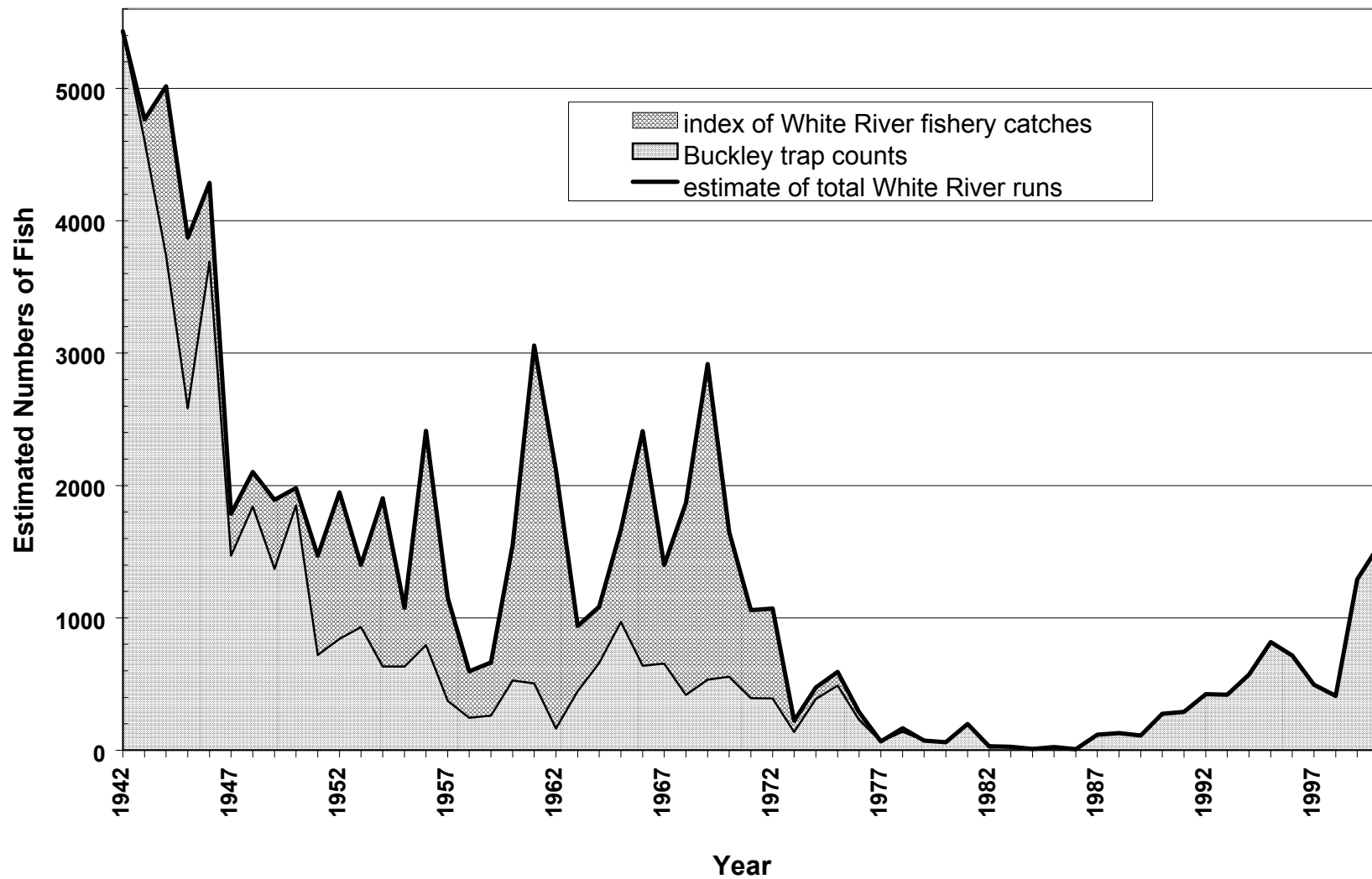
Figure 9. Buckley trap counts, estimated White River fishery catches, and estimated minimum White River runs.
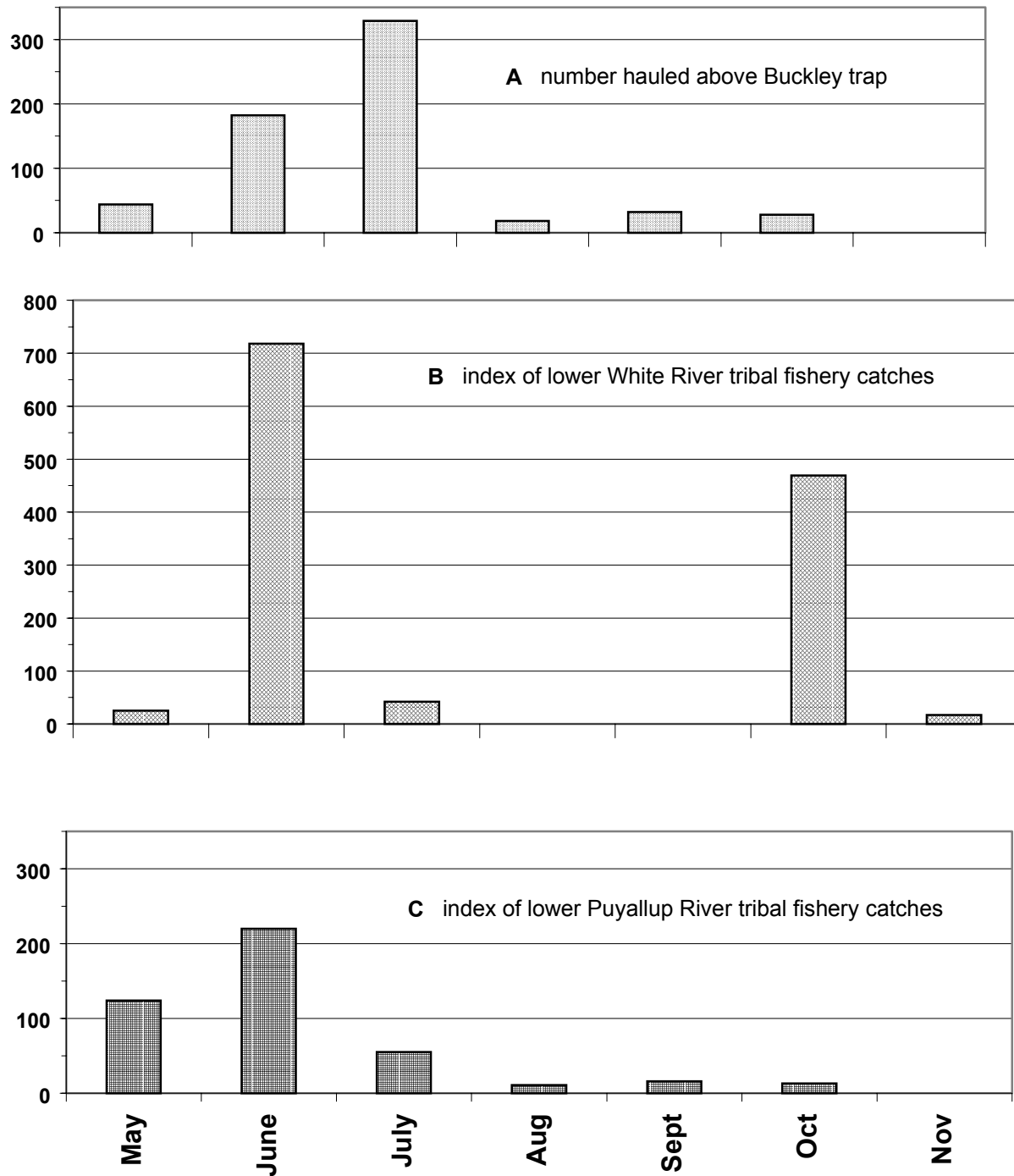
Figure 10. Estimated numbers of chinook salmon in 1954.

A actual number hauled above Buckley trap

note: 1,261 fish counted as chinook by USACE in the last two
weeks of October were excluded from this plot because they

B   index of lower White River tribal fishery catches

C   index of lower Puyallup River tribal fishery catches

May   June   July   Aug   Sept   Oct   Nov
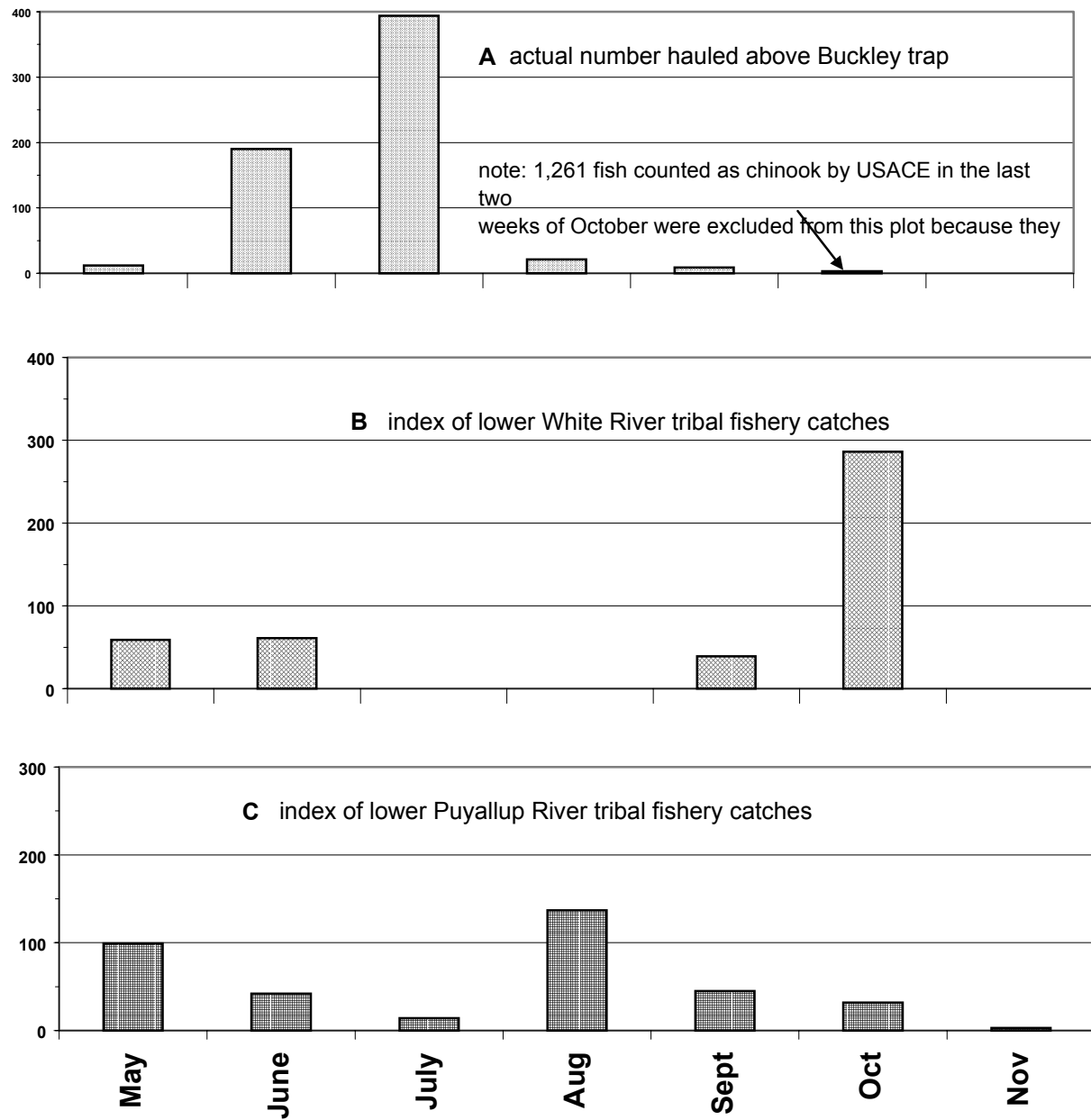
Figure 11. Estimated numbers of chinook salmon in 1955.
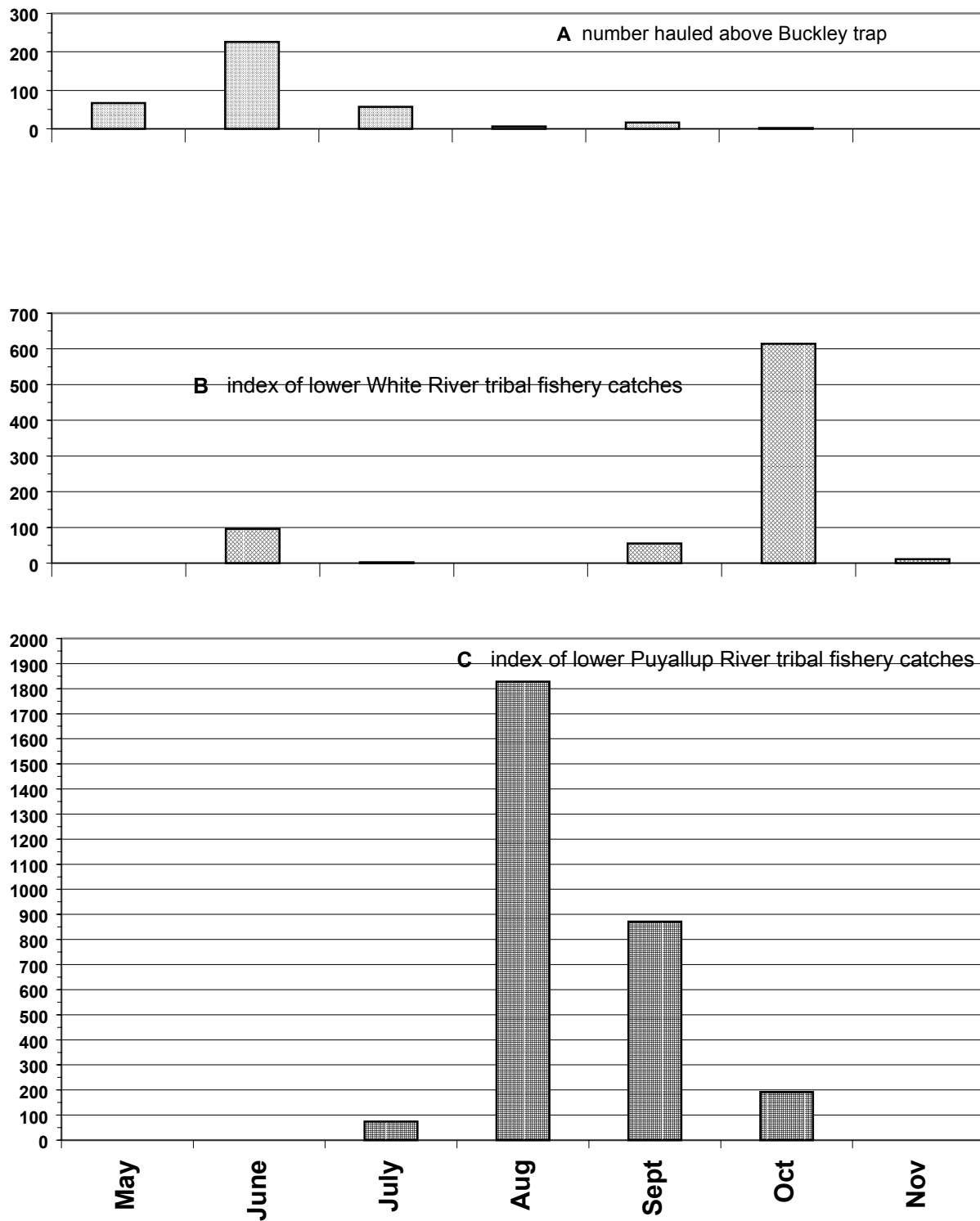
Figure 12. Estimated numbers of chinook salmon in 1957.
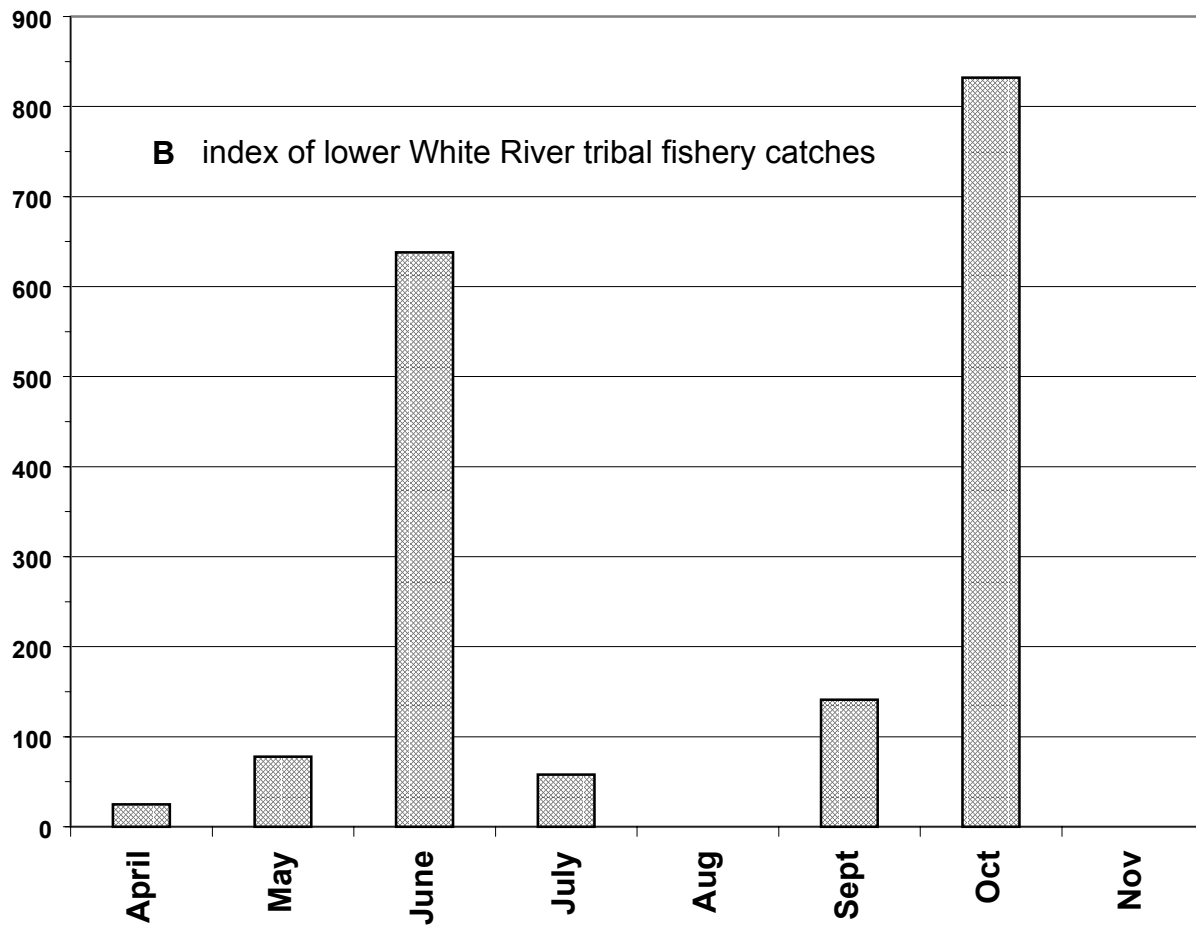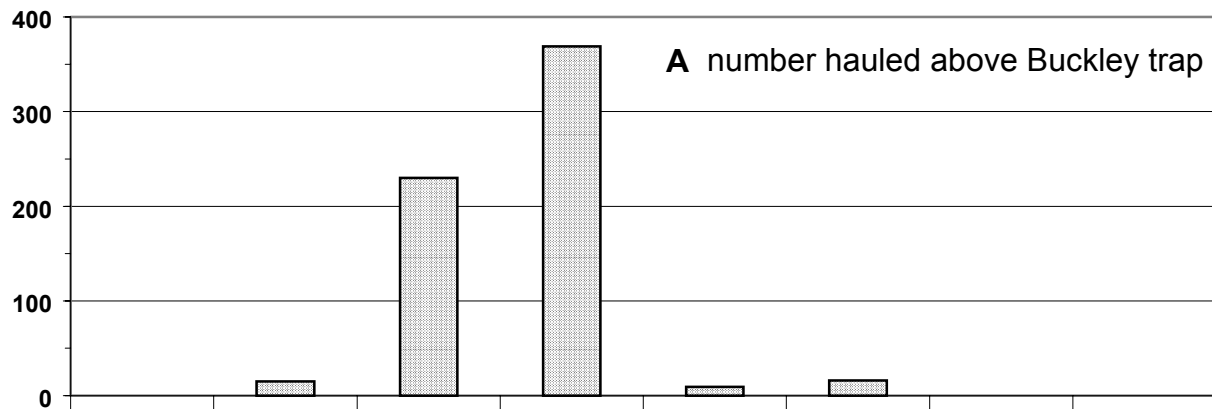
Figure 13. Estimated numbers of chinook salmon in 1966. (note: WDFW has no record of a lower Puyallup River tribal fishery in 1966.)
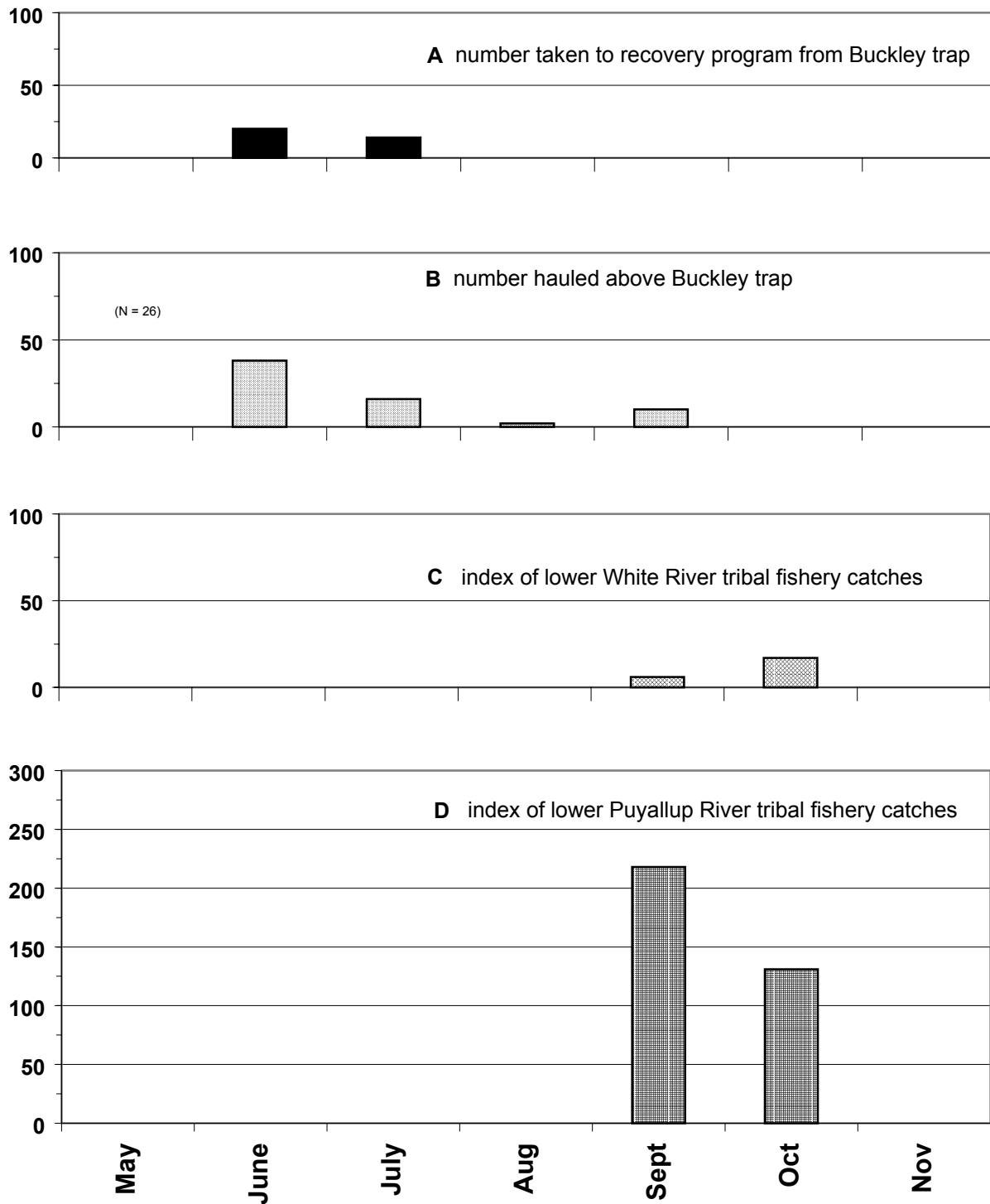
Figure 14. Estimated numbers of chinook salmon in 1977.
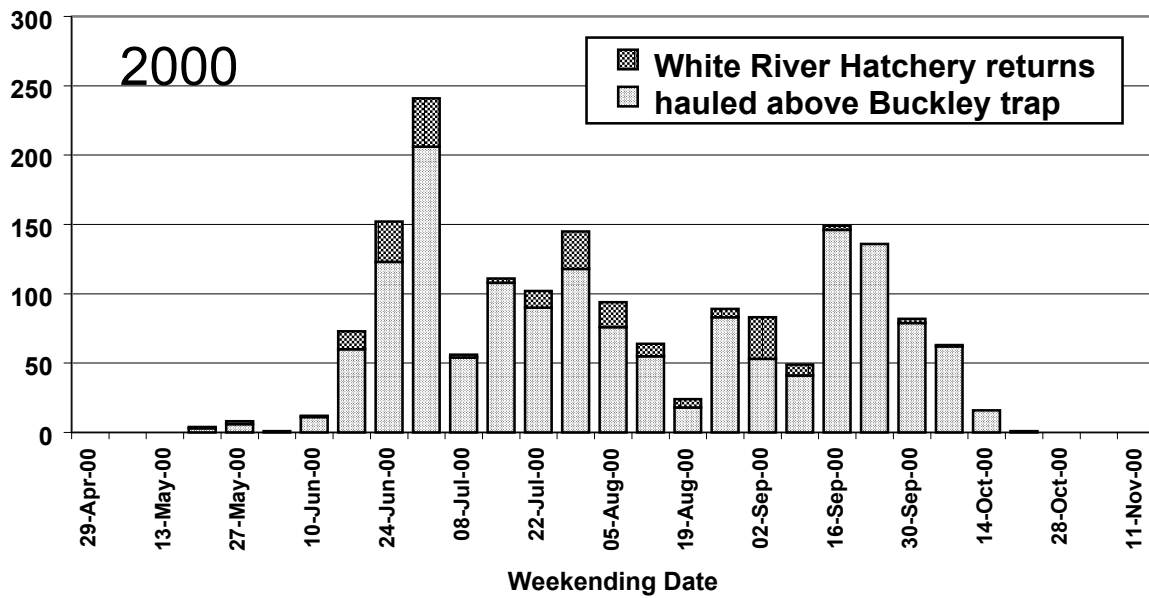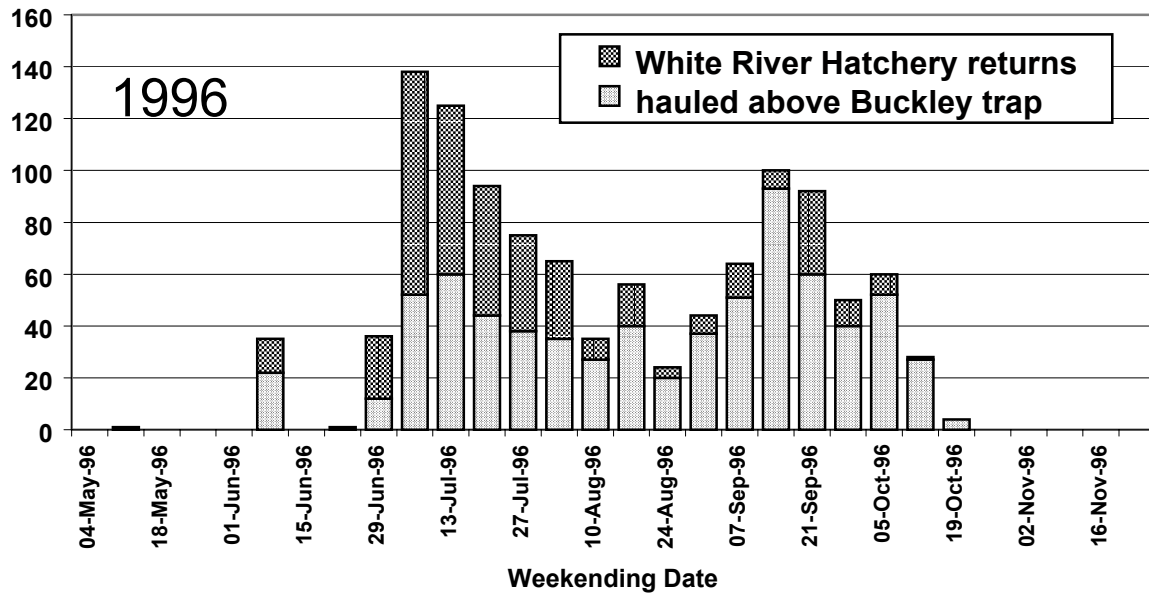
Figure 15. Numbers of White River chinook salmon in 1996 and 2000.

Appendix Table 1. Chronology of the White River System & Chinook Recovery Efforts

Date(s)	Event	Source
1887-1900	lower White River channel shifted back and forth between Green and Stuck River valleys	Salo and Jagielo, 1983
1901	WDFW Soos Creek Hatchery completed	Salo and Jagielo, 1983
1906	major flood diverted the lower White River into the Stuck River	Salo and Jagielo, 1983
1910	30 cfs minimum flow established for the by-pass reach of lower White River as part of water rights settlement associated with approval of diversion dam construction	Puget Power records
1910-1911	Puget Sound Power and Light constructed the diversion dam at Buckley (at RM 24.3); creating the lower river "by-pass reach" from RM 24.3 to RM 3.6)	Salo and Jagielo, 1983
1912-14??	fish ladder built on Buckley Diversion Dam	PSE drawing records (Bob Barnes, PSE)
1915	lower White River permanently diverted into Stuck River valley by diking and by construction of a diversion dam at Auburn	Salo and Jagielo, 1983
1939	beginning of construction of Mud Mountain Dam (at RM 29.6)	Salo and Jagielo, 1983
1940	trap operations began at Buckley; part of this year's fish runs were hauled above Mud Mountain Dam (for release at approx. RM 33.6)	Salo and Jagielo, 1983
1942	first full year fish were hauled from Buckley trap to upper White River above Mud Mountain Dam; Mud Mountain Lake began filling	Salo and Jagielo, 1983
1942-1947	construction of Mud Mountain Dam suspended by World War II	Salo and Jagielo, 1983
1945	beginning of truck logging in upper White River watershed	Weyerhaeuser Co.: Salo and Jagielo, 1983
1948	construction of Mud Mountain Dam completed	Salo and Jagielo, 1983
1949	fish ladder built over Tacoma pipeline crossing	PSE Nov. 1993 FERC application
1971-1972	some White River spring chinook were used for the production of interstock hybrids (with progeny planted out of basin) as part of a fishery enhancement effort	WDFW records
1974-1976	some White River spring chinook were used for hatchery production with yearling progeny planted back in the White River	WDFW records
1977-1986	White River Spring Chinook Recovery Program: intensive out-of-basin anadromous hatchery & saltwater captive brood production activities	WDFW records
1987	first complete year of 130 cfs minimum flow agreement for lower White River (in the "by-pass reach") with Muckleshoot Tribe	Muckleshoot Tribe
1989	White River Hatchery commenced operation	WDFW et al., 1996
1992	first year that adults from the recovery program returned to the White River	WDFW et al., 1996
1995	juvenile passage improvements at Mud Mountain Dam	WDFW et al., 1996
1996	juvenile passage improvements at Puget Power (Buckley) Dam	
	first year of release of program fish from acclimation ponds in the upper White River	WDFW et al., 1996
	The White River Spring Chinook Recovery Plan was approved	WDFW et al., 1996
1998	South Sound Net Pen captive brood operations terminated with planting of progeny from 1997 adult spawnings	WDFW records
1999	new 2-yr flow agreement for by-pass reach of lower White River (30 cfs: Oct-Jan; 130 cfs: Feb-June; 200 cfs July-Sept)	WDFW records

Appendix Table 2. Documented releases of hatchery chinook into the White River.

This tabulation does not include plants from the White River Spring Chinook Recovery Program or plants after 1982.

The absence of numbers before 1945 does not necessarily indicate no plants were made.

Releases		run-timing	Agency	Date(s)	Stage	Source
Year	Number					
1945	75,000	fall				1
1946	1,254,000	fall				1
1947	636,498	fall				1
1948	251,674	fall				1
1949	50,000	fall				1
1949	4,250	spring				1
1950	150,000*	fall				1
1953	5,000	fall	WDFW	May 29, 1953	fingerling	2
1955	17,279	fall	WDFW	June & July, 1955	fingerling	2
1957	440,000	fall	WDFW	March, 1957	unfed fry	2
1957	31,798	fall	WDFW	May - June, 1957	fingerling	2
1974	8,942	spring	WDFW	March 11, 1974	yearling	2
1976	8,340	spring	WDFW	February 20, 1976	yearling	2
1977	40,580	spring	WDFW	February 25, 1977	yearling	2
1978	47,525	spring	WDFW	March - April, 1978	yearling	2
1982	67,506	fall	Puyallup Tribe	May, 1982	fingerling	2

1 = Salo & Jagielo, 1983 (Appendix 1, Table 12)

2 = WDFW planting records databases FISH5094.DB & PLANTSREPORT.DB and PFMC Regional Mark Information System

* = Note: this release does not appear in the WDFW database cited above although it should if it is correct, because database FISH5094.DB should include all plants from 1950 through 1994.

Appendix Table 3. Out-of-basin coded wire tag recoveries in the White River and associated expansions based on tagging rates. [data provided by Richard Johnson, Muckleshoot Tribe]

1998

None

1999

Tag Code	Species	Run	Sex	Brood Year	Hatchery	Release Site	Release Date	Tag Rate for group	# Expected Above Trap (based on tag expansion)
63-03-12	chinook	fall	jack	1997	Voights Creek	Voights Creek	05/30/1998	13.0%	**31**
63-03-12	chinook	fall	jack	1997	Voights Creek	Voights Creek	05/30/1998		
63-03-12	chinook	fall	jack	1997	Voights Creek	Voights Creek	05/30/1998		
63-03-12	chinook	fall	jack	1997	Voights Creek	Voights Creek	05/30/1998		
63-03-07	chinook	fall	jack	1997	PTI*	Diru Creek	05/26/1998	47.8%	**2**
63-59-62	chinook	fall	female	1995		South Sound net pens	04/01/1997	39.0%	**3**
63-06-08	chinook	fall	jack	1997	McKernan	Fox Island net pens	01/31/1999	100.0%	**3**
63-06-08	chinook	fall	jack	1997	McKernan	Fox Island net pens	01/31/1999		
63-06-08	chinook	fall	jack	1997	McKernan	Fox Island net pens	01/31/1999		
63-07-45	chinook	fall	jack	1997	Marblemount	Elliott Bay N.P.	Spring 1999	100.0%	**2**
63-07-45	chinook	fall	jack	1997	Marblemount	Elliott Bay N.P.	Spring 1999		
21-30-44	chinook	spring	male	1996	Battle Creek	Mission Creek	04/29/1998	98.6%	**1**
63-06-07	chinook	fall	jack	1997	Hoodsport	Hoodsport	May 1999	100.0%	**1**

*PTI = Puyallup Tribe of Indians

*

Appendix Table 4. Numbers of chinook graphed in various figures (blanks indicated no information, not zero).

Year	Total number of chinook (adults + jacks) arriving at the Buckley trap[1]	Number arriving at Buckley trap after 2nd week of August[2]	Total estimated catch in the lower White River tribal fishery[3]	Estimated minimum run to the White River[4]	Total estimated catch in the lower Puyallup River tribal fishery[3]
1940	no count				
1941	partial				
1942	5,431				5,431
1943	4,603		162	4,765	
1944	3,736		1,281	5,017	
1945	2,584		1,289	3,873	
1946	3,692		595	4,287	
1947	1,470		317	1,787	
1948	1,841		261	2,102	
1949	1,370		521	1,891	
1950	1,849		132	1,981	
1951	719		750	1,469	
1952	842		1,106	1,948	
1953	931		471	1,402	
1954	633	67	1,271	1,904	439
1955	632	18	445	1,077	372
1956	794	33	1,619	2,413	824
1957	374	24	778	1,152	2,965
1958	245	14	351	596	2,058
1959	261	56	403	664	2,562
1960	528	20	1,026	1,554	5,229
1961	505	21	2,553	3,058	10,659
1962	164	12	1,952	2,116	5,813
1963	447	26	491	938	7,985
1964	658	20	426	1,084	3,746
1965	969	12	697	1,666	675
1966	639	18	1,772	2,411	
1967	654	26	745	1,399	1
1968	417	35	1,450	1,867	
1969	534	17	2,384	2,918	136
1970	557	24	1,096	1,653	493

Year	Total number of chinook (adults + jacks) arriving at the Buckley trap[1]	Number arriving at Buckley trap after 2nd week of August[2]	Total estimated catch in the lower White River tribal fishery[3]	Estimated minimum run to the White River[4]	Estimated White River sport fishery catches[5]	Total estimated catch in the lower Puyallup River tribal fishery[3]	Number transferred from the Buckley trap to the Recovery Program[6]	Number of Buckley trap origin fish spawned in the Recovery Program[7]
1971[11]	393	15	666	1,059		1,233		
1972[9,11]	392	47	678	1,070		2,794		
1973[9]	136	87	86	222		2,211		
1974[11]	388	48	87	475	3	2,649		
1975[11]	488	172	104	592	0	1,699		
1976[11]	229	16	59	288	0	345		
1977[12]	66	10	0	66	0	353	34	26
1978	140	115	27	167	11	392	25	8
1979	72	6		72	nd	1,626	33	30
1980	61	14		61	0	396	42	38
1981[13]	199	174		199	4	546	23	22
1982[14]	20	7	11	31	0	354	13	13
1983	26	2	1	27	0	809	24	22
1984[15]	10	3		10	0	651	7	2
1985	24	24		24	2	775	0	0
1986	8	6		8	5	843	3	2
					Recovery Program totals =		**204**	**163**
1987	117	116		117	16	1,304		
1988	129	118		129	2	1,307		
1989	111	77		111	0	660		
1990	275	221		275	33	1,125		
1991	290	276		290	3	576		
1992[16]	424	348		424	3	718		
1993[17]	419	386		419	0	1,705		
1994[18]	571	521		571	0	3,566		
1995	813	647		817	4	5,001		
1996[17]	715	384		715	7	4,886		
1997	494	200		494	3	2,700		
1998	402	189		412	10	1,581		
1999	1,291	541		1,291	0	1,884		
2000	1,546	635		1,545				

1 = Buckley trap counts from USACE weekly & summary records (note that the counts for 1954 - 1975 were "verified" from handwritten weekly trap records in the WDFW Habitat Management Program and may represent "adult only" counts because no jacks were recorded in these years).

2 = counts for 1954 - 1975 from handwritten weekly Buckley trap summary records in WDFW Habitat Management Program

3 = from official WDF salmon fishery catch statistics, published WDF Fishery Statistical Reports and the WDFW GIMLI/HCCE database

4 = total number at Buckley trap + total catch in the lower White River tribal fishery

5 = numbers are expanded and bias-adjusted estimates from punch cards; no chinook-specific data prior to 1974; from WDFW Washington State Sport Catch Reports

6 = numbers derived from USACE Buckley trap records and WDFW Form 152s

7 = numbers derived from WDFW Form 152s and 152-As

8 = total USACE Buckley trap count corrected for 1,261 presumed coho; based on WDFW handwritten weekly Buckley trap records in WDFW Habitat Management Program; count includes 3 fish that arrived after November 19th (see Appendix Table 6 for details).

9 = total USACE Buckley trap count corrected based on WDFW handwritten weekly Buckley trap records in the WDFW Habitat Management Program

10 = estimated lower Puyallup River tribal catch (N = 136) from official WDF salmon fishery catch statistics, not published WDF Fishery Statistical Reports (N = 132)

11 = tabulated counts probably do not include fish taken for hatchery programs (N = 52 in 1971; N = 53 in 1972; N = 38 in 1974; N = 21 in 1975; and N = 44 in 1976,

12 = estimated lower White River tribal catch (N = 0) according to internal memo of Geist & Flint correcting published WDF Fishery Statistical Report (N = 23)

13 = note that the Buckley trap count includes 1 fish that arrived in March and 97 fish that arrived after October 24th

14 = note that the Buckley trap count includes 3 fish that arrived after December 1st

15 = note that the Buckley trap count includes 1 fish shown only on WDFW hatchery records

16 = total USACE Buckley trap count corrected from weekly USACE records; incudes 11 fish in December

17 = total USACE Buckley trap count corrected from weekly USACE records

18 = total USACE Buckley trap count corrected from weekly USACE records (note: count includes 1 fish arriving in January)

Appendix Table 5. Details of primers and PCR conditions used in this study.

A. Primer Sequences and Sources

Locus	Forward (5'→3')	Reverse (5' →3')	Literature Citation
Omy-325	TgT gAg ACT gTC AgA TTT TgC	Cgg AgT CCg TAT CCT TCC C	O'Connell, M. (pers. comm. via Jeff Olsen, ADFG)
One-8	AAC ATT CTg ggA TgA CAg ggg TA	CTg TTC TgC TCC AgT gAA gTg gA	Scribner et al., 1996. Can. J. Fish. Aquat. Sci. 53:833-841
Ots-100	TgA ACA TgA gCT gTg TgA g	ACg gAC gTg CCA gTg Ag	Nelson & Beacham 1999. Anim. Genet. 30:228-229
Ocl-1	ACT ACT AAC CAg CCC ACC ACC C	AgA CAg AgA ggg Agg gAA gC	Condrey & Bentzen 1998. Mol. Ecol. 7:787-789
Ots-101	ACg TCT gAC TTC AAT gAT gTT T	TAT TAA TTA TCC TCC AAC CCA g	Small et al., 1998. Mol. Ecol. 7:141-155
Ots-102	Agg ATC AAA TAA ggA gTg ATA	ACT Agg TAT CCC CTT AAC CA	Nelson & Beacham 1999. Anim. Genet. 30:228-229
Ots-104	gCA CTg TAT CCA CCA gTA	gTA ggA gTT TCA TTT gAA TC	Nelson & Beacham 1999. Anim. Genet. 30:228-229
Ots-2	ACA CCT CAC ACT TAg A	AAT ATC CTT CAC ACT g	Banks et al., 1999. J. Hered. 90:281-288 (with errata sheet)
Ots-3	CAC ACT CTT TCA ggA g	AgA ATC ACA ATg gAA g	Banks et al., 1999. J. Hered. 90:281-288 (with errata sheet)
One-10	ATg ggg AAC AgA AgA ggA AT	CTg TAg gTg TgA AAT gTA TTT AAA	Scribner et al., 1996. Can. J. Fish. Aquat. Sci. 53:833-841
Ogo-2	ACA TCg CAC ACC ATA AgC AT	gTT TCT TCg ACT gTT TCC TCT gTg TTg Ag	Olsen et al., 1998. Mol. Ecol. 7:1083-1090
Ogo-4	gTC gTC ACT ggC ATC AgC TA	gAg Tgg AgA TgC AgC CAA Ag	Olsen et al., 1998. Mol. Ecol. 7:1083-1090
Ots-1	ggA AAg AgC AgA TgT TgT T	TgA AgC AgC AgA TAA AgC A	Banks et al., 1999. J. Hered. 90:281-288 (with errata sheet)
Ots-108	TTT CTA TTA gTC TgT CAC TAC	Tgg CAA ggA gAg ACA gAg gg	Nelson & Beacham 1999. Anim. Genet. 30:228-229
Ots-107	ACA gAC CAg ACC TCA ACA	ATA gAg ACC TgA ATC ggT A	Nelson & Beacham 1999. Anim. Genet. 30:228-229
Ssa-197	ggg TTg AgT Agg gAg gCT Tg	Tgg CAg ggA TTT gAC ATA AC	O'Reilly et al., 1996. Can. J. Fish. Aquat. Sci. 53:2292-2298
Str-60	Cgg TgT gCT TgT CAg gTT TC	gTC AAg TCA gCA AgC CTC AC	Estoup et al., 1993. Heredity 71:488-496
Str-73	CCT ggA gAT CCT CCA gCA ggA	CTA TTC TgC TTg TAA CTA gAC CTA	Estoup et al., 1993. Heredity 71:488-496

**B. Multiplex PCR conditions** (TD = touchdown PCR)

K1 (2.25 mM MgCl$_2$; 63-59EC TD; 35 cycles at 58EC; 30 m at 72EC) – *0.07 μM Omy-325* (ned); 0.08 *μM One-8* (ned); 0.09 *μM Ots-100* (ned); 0.05 *μM Ocl-1*(hex)

K2Aa (2.5 mM MgCl$_2$; 54-49EC TD; 24 cycles at 49EC; 30 m at 72EC) – 0.2 *μM Ots-101* (6-fam); 0.5 *μM Ots-102* (ned)

K2Ab (2.5 mM MgCl$_2$; 54-49EC TD; 29 cycles at 49EC; 30 m at 72EC) – *0.5 μM Ots-104* (hex)

K2Ba (2.0 mM MgCl$_2$; 54-49EC TD; 24 cycles at 49EC; 30 m at 72EC) – 0.263 *μM Ots-2* (6-fam); 0.263 *μM Ots-3* (ned)

K2Bb (2.0 mM MgCl$_2$; 54-49EC TD; 24 cycles at 49EC; 30 m at 72EC) – 0.112 *μM One-10* (hex)

K3 (2.25 mM MgCl$_2$; 63-59EC TD; 19 cycles at 58EC; 30 m at 72EC) – 0.063 *μM Ogo-2* (6-fam); 0.174 *μM Ogo-4* (hex)

K4a (2.0 mM MgCl$_2$; 54-49EC TD; 36 cycles at 49EC; 30 m at 72EC) – 0.5 *μM Ots-1* (6-fam); 0.5 *μM Ots-108* (ned)

K4b (2.0 mM MgCl$_2$; 54-49EC TD; 36 cycles at 49EC; 30 m at 72EC) – 0.5 *μM Ots-107* (hex)

K5a (2.25 mM MgCl$_2$; 63-58EC TD; 19 cycles at 58EC; 30 m at 72EC) – 0.062 *μM Ssa-197* (6-fam)

K5b (1.5 mM MgCl$_2$; 63-58EC TD; 19 cycles at 58EC; 30 m at 72EC) – 0.15 *μM Str-60* (ned); *0.192 μM Str-73* (hex)

Appendix Table 6. Original USACE counts of chinook and coho at the Buckley trap in 1955 as recorded at WDFW and Shaklee's and Young's "corrections" for presumed recording erros in two weeks in late October.

| Week ending date	USACE counts at Buckley trap (as recorded at WDFW)		Shaklee and Young "corrected counts"	
	chinook	coho	chinook	coho
Prior to 30-Apr		111		111
30-Apr				
07-May				
14-May				
21-May	8		8	
28-May	4		4	
04-Jun	7		7	
11-Jun	38		38	
18-Jun	9		9	
25-Jun	136		136	
02-Jul	126		126	
09-Jul	84		84	
16-Jul	114		114	
23-Jul	45		45	
30-Jul	25		25	
06-Aug	11		11	
13-Aug	7		7	
20-Aug				
27-Aug	3		3	
03-Sep	4	1	4	1
10-Sep	2	3	2	3
17-Sep	3	3	3	3
24-Sep				
01-Oct	1	9	1	9
08-Oct	2	23	2	23
15-Oct		1310		1310
22-Oct	**<u>799</u>**			**<u>799</u>**
29-Oct	**<u>462</u>**			**<u>462</u>**
05-Nov		45		45
12-Nov		199		199
19-Nov				
26-Nov	3		3	
03-Dec		86		86
10-Dec		54		54
17-Dec		63		63
24-Dec		54		54
31-Dec				
Totals	1893	1961	632	3222

Appendix Figure 1. Map of the Puyallup River Basin
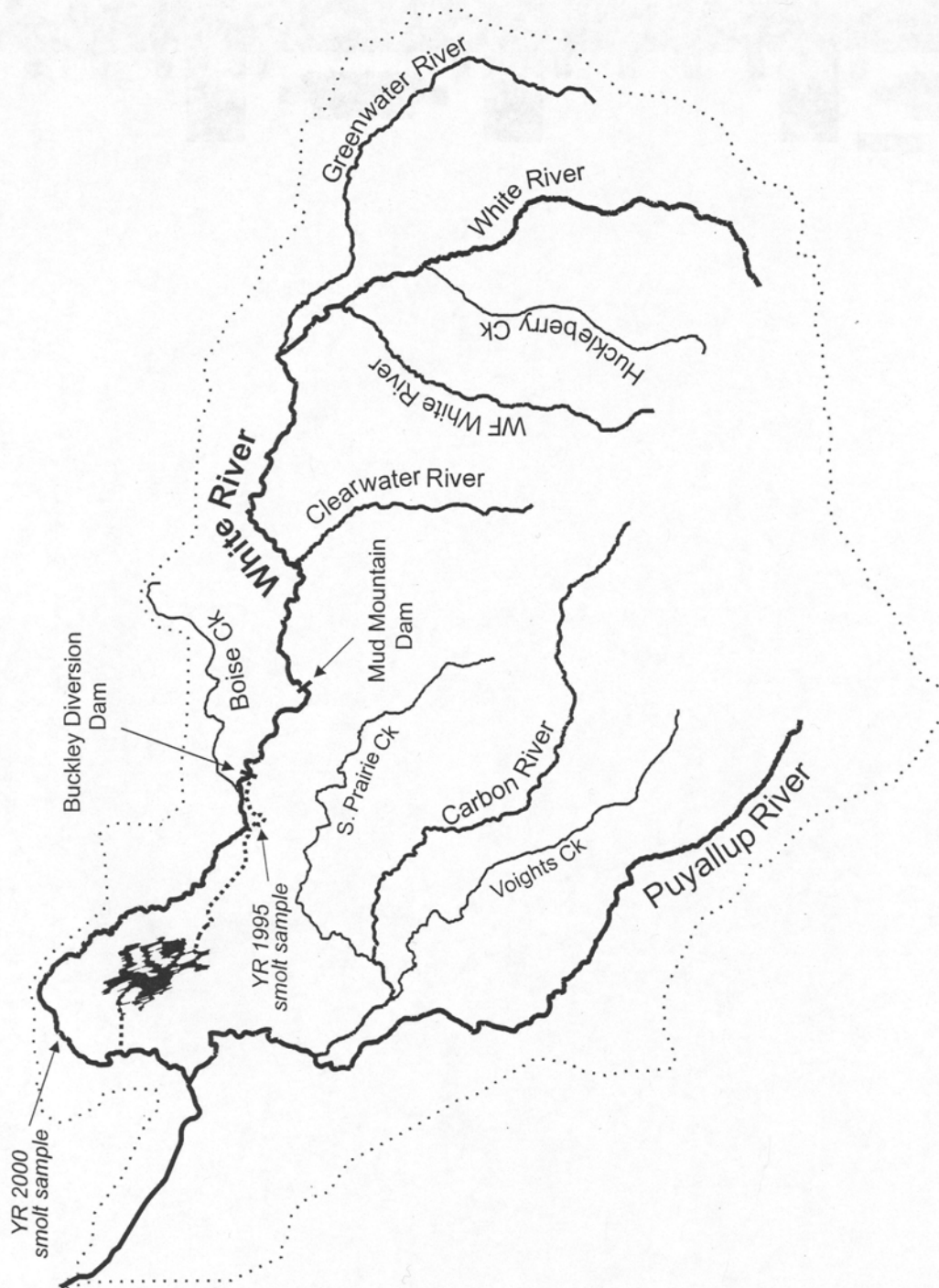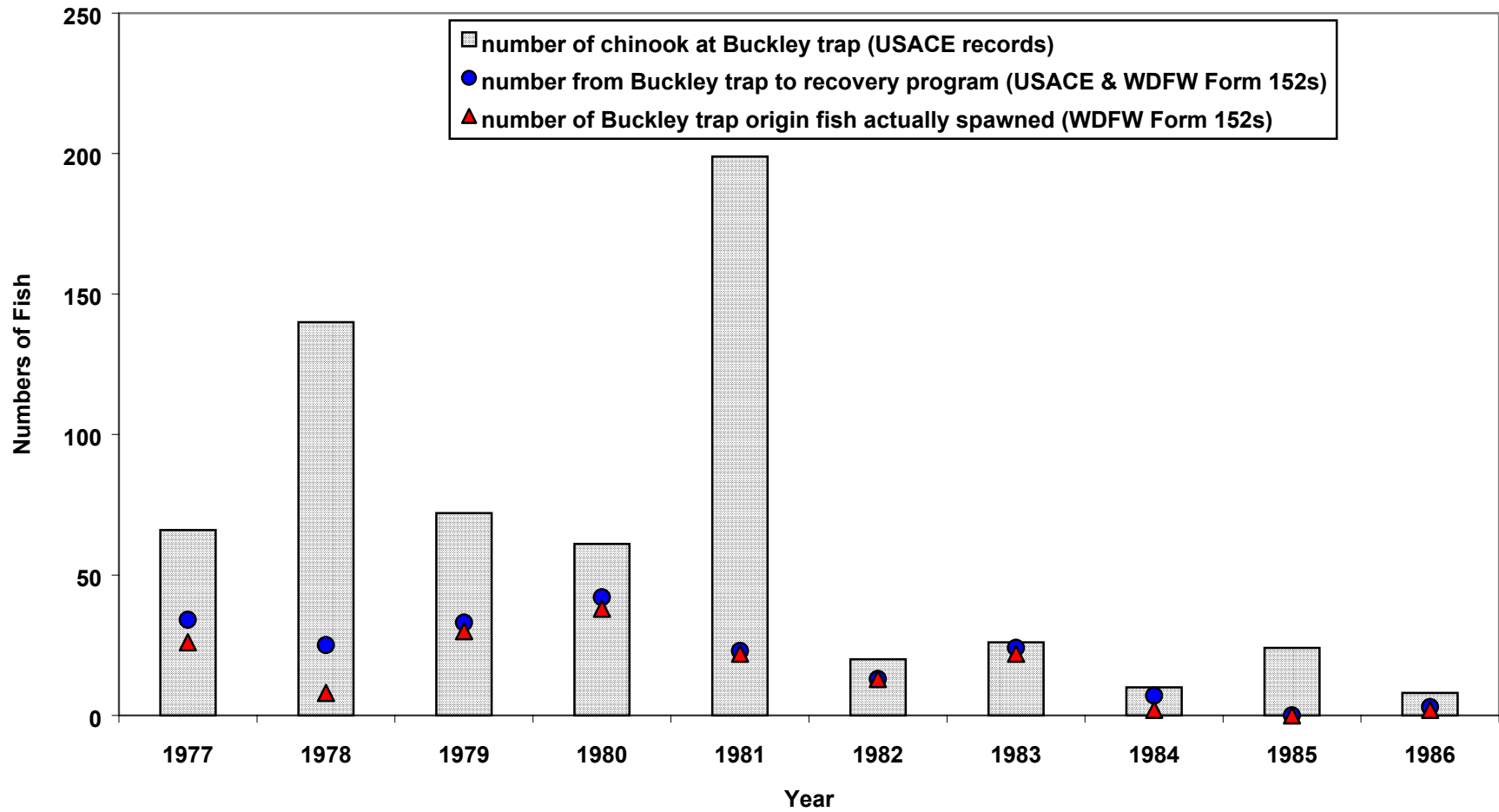
Appendix Figure 2. Numbers of fish used in the White River Spring Chinook Recovery Program (1977-1986).
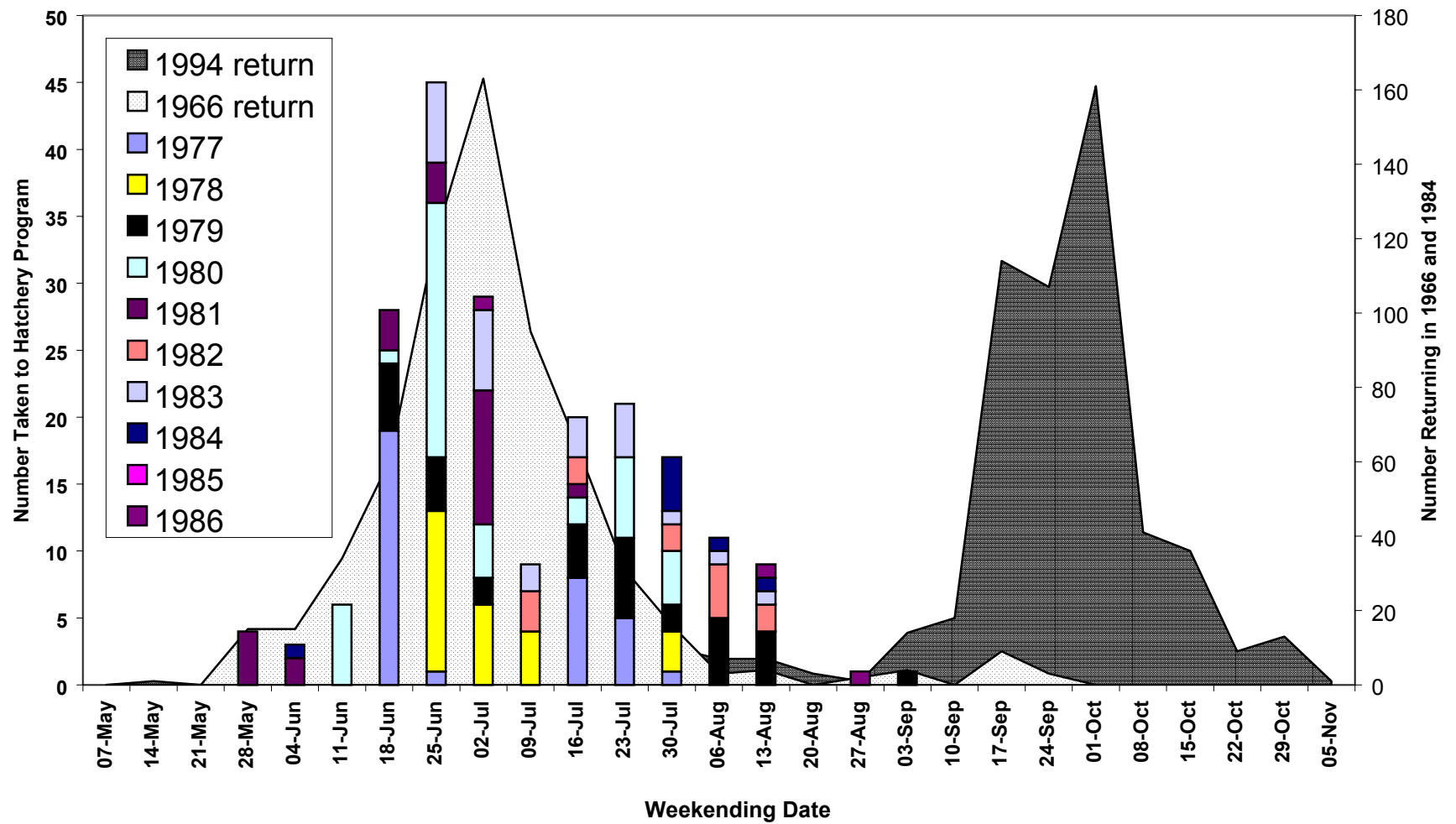
Appendix Figure 3. Weekly return-timing of fish from Buckley trap taken to the Recovery Program (1977-1986) compared to return timing of total run in 1966 ("spring-type") and total run in 1994 (fall-type).